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JUN 02 2003
TECH CENTER 1600/2900

Tue Apr 1 16:16:15 2003 [BLASTP 2.2.2 [Jan-08-2002], NCBI]

/home/glinda/vf/Legal/byeung/pl.DNA40370 (452 aa)

/home/glinda/vf/Legal/byeung/pl.DNA40370

Database: day (2,655,410 seqs, 680,241,903 aa) Mar 24, 2003 2:54 PM

Locus list: hum (596,938 seqs, 114,350,192 aa)

Matrix: BLOSUM62, T: 11, A: 40, X1: 16, X2: 38, X3: 64, S1: 41, S2: 75, eval: 10.

Gap Penalties: Existence: 11, Extension: 1

Sequences producing High-scoring Segment Pairs:		Score	Match	Pct	E-val
1	P_ABB84842 Human PRO302 protein sequence SEQ ID NO:52	2382	452	100	0.0
2	P_ABB95448 Human angiogenesis related protein PRO302	2382	452	100	0.0
3	P_ABP65102 Hypoxia-induced protein #28 - Homo sapiens	2382	452	100	0.0
4	P_ABB99215 Human retinoid inducible serine carboxypep	2382	452	100	0.0
5	P_AAB80255 Human PRO302 protein - Homo sapiens.	2382	452	100	0.0
6	P_AAB20341 Human PRO302 - Homo sapiens.	2382	452	100	0.0
7	P_AAB93913 Human protein sequence SEQ ID NO:13882 - H	2382	452	100	0.0
8	P_AAE06595 Human protein having hydrophobic domain, H	2382	452	100	0.0
9	P_AAY88378 PRO302, vitellogenic carboxypeptidase homo	2382	452	100	0.0
10	P_AAY13387 protein PRO302 - Homo sapiens.	2382	452	100	0.0
11	P_AAY05768 Human PRO216 (vitellogenic carboxypeptidas	2382	452	100	0.0
12	CAC51169.1 unnamed protein product - Homo sapiens	2382	452	100	0.0
13	AAG16692.1 serine carboxypeptidase 1 precursor protei	2382	452	100	0.0
14	BAB55069.1 unnamed protein product - Homo sapiens	2382	452	100	0.0
15	NP_067639.1 serine carboxypeptidase 1 precursor protei	2382	452	100	0.0
16	RISC_HUMAN Retinoid-inducible serine carboxypeptidase	2382	452	100	0.0
17	P_AAU96225 Human secreted protein, SEQ ID No 127 - Ho	2372	451	100	0.0
18	P_AAB41675 Human ORFX ORF1439 polypeptide sequence SE	2306	439	97	0.0
19	AAG39285.1 MSTP034 - Homo sapiens	2116	402	100	0.0

>1 P_ABB84842 Human PRO302 protein sequence SEQ ID NO:52 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
P_ABB84842	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
P_ABB84842	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
P_ABB84842	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
P_ABB84842	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATLWGAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
P_ABB84842	241	VNKGLYREATLWGAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
P_ABB84842	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

```

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_ABB84842 361 INVTVYNGQLDLIVDTMGQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_ABB84842 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>2 P_ABB95448 Human angiogenesis related protein PRO302 SEQ ID NO: 52 - Homo (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_ABB95448 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNVPVGT
*****
P_ABB95448 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNVPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_ABB95448 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_ABB95448 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_ABB95448 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_ABB95448 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_ABB95448 361 INVTVYNGQLDLIVDTMGQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_ABB95448 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>3 P_ABP65102 Hypoxia-induced protein #28 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_ABP65102 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNVPVGT
*****
P_ABP65102 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNVPVGT

```

```

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AB P65102 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AB P65102 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AB P65102 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AB P65102 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
DNA40370 361 INVTVYNGQLDLIVDTMGQEA WVRKLKWPPEL PKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AB P65102 361 INVTVYNGQLDLIVDTMGQEA WVRKLKWPPEL PKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
DNA40370 421 LAFYWILKAGHMVPSDQGD MALKMMRLVTQQE
*****
P_AB P65102 421 LAFYWILKAGHMVPSDQGD MALKMMRLVTQQE
*****

```

>4 P_ABB99215 Human retinoid inducible serine carboxypeptidase - Homo (452 aa)
[1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AB B99215 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AB B99215 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AB B99215 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AB B99215 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AB B99215 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AB B99215 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
DNA40370 361 INVTVYNGQLDLIVDTMGQEA WVRKLKWPPEL PKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AB B99215 361 INVTVYNGQLDLIVDTMGQEA WVRKLKWPPEL PKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
DNA40370 421 LAFYWILKAGHMVPSDQGD MALKMMRLVTQQE
*****

```

P_ABB99215 421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>5 P_AAB80255 Human PRO302 protein - Homo sapiens. (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

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DNA40370      1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB80255     1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370     61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB80255     61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_AAB80255    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB80255    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370    241 VNKGLYREATLWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB80255    241 VNKGLYREATLWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370    301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB80255    301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370    361 INVTVYNGQLDLIVDTMQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSFVKSYKN
*****
P_AAB80255    361 INVTVYNGQLDLIVDTMQEAWVRKCLKWPELKFSQLKWKALYSDPKSLETSFVKSYKN

DNA40370    421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE
*****
P_AAB80255    421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE
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>6 P_AAB20341 Human PRO302 - Homo sapiens. (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

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DNA40370      1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB20341     1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370     61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB20341     61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_AAB20341    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB20341    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
```



```

DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB20341 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB20341 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAB20341 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE
*****
P_AAB20341 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE

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>7 P_AAB93913 Human protein sequence SEQ ID NO:13882 - Homo sapiens. (452 aa) [1 seg]

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Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB93913 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB93913 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****
P_AAB93913 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB93913 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB93913 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB93913 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAB93913 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE
*****
P_AAB93913 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE

```

>8 P_AAE06595 Human protein having hydrophobic domain, HP03959 - Homo (452 aa) [1 seg]

```

Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

```

DNA40370      1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAE06595    1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370      61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAE06595    61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370      121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAE06595    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370      181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAE06595    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370      241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRH
*****
P_AAE06595    241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRH

DNA40370      301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAE06595    301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370      361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAE06595    361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370      421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAE06595    421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>9 P_AAY88378 PRO302, vitellogenic carboxypeptidase homologue amino acid
sequence - Homo sapiens. (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370      1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAY88378    1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370      61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAY88378    61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370      121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAY88378    121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370      181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY88378    181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370      241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRH
*****
P_AAY88378    241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRH

```

```

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY88378 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY88378 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAY88378 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>10 P_AAY13387 protein PRO302 - Homo sapiens. (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAY13387 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAY13387 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_AAY13387 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370 181 YKAIQRTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY13387 181 YKAIQRTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY13387 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY13387 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY13387 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAY13387 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>11 P_AAY05768 Human PRO216 (vitellogenic carboxypeptidase homologue) - Homo
(452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAY05768 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT

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*****
P_AAY05768 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_AAY05768 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY05768 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY05768 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY05768 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY05768 361 INVTYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAY05768 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>12 CAC51169.1 unnamed protein product - Homo sapiens (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
CAC51169.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
CAC51169.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
CAC51169.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
CAC51169.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
CAC51169.1 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
CAC51169.1 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
CAC51169.1 361 INVTYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

```

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

 CAC51169.1 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>13 AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

 AAG16692.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
 DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

 AAG16692.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
 DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

 AAG16692.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
 DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

 AAG16692.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
 DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

 AAG16692.1 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
 DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

 AAG16692.1 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
 DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN

 AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN
 DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

 AAG16692.1 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>14 BAB55069.1 unnamed protein product - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

 BAB55069.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
 DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

 BAB55069.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
 DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

 BAB55069.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

 BAB55069.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
 DNA40370 241 VNKGlyREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

 BAB55069.1 241 VNKGlyREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
 DNA40370 301 VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

 BAB55069.1 301 VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
 DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

 BAB55069.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
 DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

 BAB55069.1 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>15 NP_067639.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

 NP_067639.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
 DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

 NP_067639.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
 DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

 NP_067639.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
 DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

 NP_067639.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
 DNA40370 241 VNKGlyREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

 NP_067639.1 241 VNKGlyREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
 DNA40370 301 VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

 NP_067639.1 301 VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
 DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN

 NP_067639.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKN
 DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

 NP_067639.1 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>16 RISC_HUMAN Retinoid-inducible serine carboxypeptidase precursor
 /pid=AAG16692.1 - homo sapiens (452 aa) [1 seg]
 Score = 2382 (922 bits), Expect = 0.0
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

RISC_HUMAN	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

RISC_HUMAN	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

RISC_HUMAN	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

RISC_HUMAN	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

RISC_HUMAN	241	VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

RISC_HUMAN	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370	361	INVTVYNGQLDLIVDTMGQEAWRKCLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYN

RISC_HUMAN	361	INVTVYNGQLDLIVDTMGQEAWRKCLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYN
DNA40370	421	LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

RISC_HUMAN	421	LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>17 P_AAU96225 Human secreted protein, SEQ ID No 127 - Homo sapiens. (452 aa) [1 seg]
 Score = 2372 (918 bits), Expect = 0.0
 Identities = 451/452 (99%), Positives = 451/452 (99%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

P_AAU96225	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

P_AAU96225	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKLRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

P_AAU96225	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

P_AAU96225	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

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DNA40370 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAU96225 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAU96225 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKWKPELPKFSQKWKALYSDPKSLETSAFVKSYKN
*****
P_AAU96225 361 INVTVYNGQLDLIVDTMGQEAWVRKWKPELPKFSQKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE
*****
P_AAU96225 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE

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>18 P_AAB41675 Human ORFX ORF1439 polypeptide sequence SEQ ID NO:2878 - Homo (451 aa) [1 seg]
Score = 2306 (892 bits), Expect = 0.0
Identities = 439/452 (97%), Positives = 444/452 (98%), Gaps = 1/452 (0%), at 1,1-452,451

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB41675 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATT

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB41675 61 PART-SELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****
P_AAB41675 120 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB41675 180 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB41675 240 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB41675 300 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVIDIVDTLLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKWKPELPKFSQKWKALYSDPKSLETSAFVKSYKN
*****
P_AAB41675 360 VNVTVYNGQLDLIVDTIGQEAWVRKWKPELSRFNQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE
*****
P_AAB41675 420 LAFYWILKAGHMVPSDQGDMMALKMMRLVTQQE

```

>19 AAG39285.1 MSTP034 - Homo sapiens (402 aa) [1 seg]
Score = 2116 (819 bits), Expect = 0.0
Identities = 402/402 (100%), Positives = 402/402 (100%), at 51,1-452,402

DNA40370 51 MFWWLYYATNSCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAAS

 AAG39285.1 1 MFWWLYYATNSCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAAS

 DNA40370 111 LLFVDNPVGTGFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGG

 AAG39285.1 61 LLFVDNPVGTGFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGG

 DNA40370 171 KMAAGIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEV

 AAG39285.1 121 KMAAGIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEV

 DNA40370 231 SKVAEQVLNAV NKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQ

 AAG39285.1 181 SKVAEQVLNAV NKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQ

 DNA40370 291 SHLVCLCQRHVRHLQDALS QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVI

 AAG39285.1 241 SHLVCLCQRHVRHLQDALS QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVI

 DNA40370 351 SIVDELLEAGINVTVYNGQLDLIVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLE

 AAG39285.1 301 SIVDELLEAGINVTVYNGQLDLIVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLE

 DNA40370 411 TSAFVKSYKNLAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE

 AAG39285.1 361 TSAFVKSYKNLAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE

Dayhoff Protein Database (Rel 75, Feb 2003)

P_ABB84842 Human PRO302 protein sequence SEQ ID NO:52 - Homo sapiens.

Length: 452 aa

Accession: P_ABB84842;

Species: Homo sapiens.

Keywords: Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; patent; GENESEQ patentdb.

Patent number: WO200200690-A2.

Publication date: 03-JAN-2002.

Filing date: 20-JUN-2001; 2001WO-US19692.

Priority: 23-JUN-2000; 2000US-213637P. 20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220624P.30-MAY-2001; 2001WO-US17443.

01-JUN-2001; 2001WO-US17800. plus 32 more dates.

Assignee: (GETH) GENENTECH INC.

Inventors: Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

Cross reference: WPI; 2002-090516/12. N-PSDB; ABL88097.

Title: One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

Patent format: Claim 11; Fig 52; 565pp; English.

Comment: ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

Database: GENESEQ patent database.

P_ABB95448 Human angiogenesis related protein PRO302 SEQ ID NO: 52 - Homo sapiens.

Length: 452 aa

Accession: P_ABB95448;

Species: Homo sapiens.

Keywords: Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; patent; GENESEQ patentdb.

Patent number: WO200208284-A2.
 Publication date: 31-JAN-2002.
 Filing date: 09-JUL-2001; 2001WO-US21735.
 Priority: 20-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-220624P.
 25-JUL-2000; 2000US-220664P. 20-JUN-2001; 2001WO-US19692.
 28-JUN-2001; 2001WO-US00000. plus 34 more dates.
 Assignee: (GETH) GENENTECH INC. (BAKE/) BAKER K P. (FERR/) FERRARA N.
 (GERB/) GERBER H. (GERR/) GERRITSEN M E. (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (HILL/) HILLAN K J. (MARS/) MARSTERS S A. (PANJ/) PAN J. (PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C K. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I.
 Inventors: Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 Cross reference: WPI; 2002-171999/22. N-PSDB; ABL95586.
 Title: One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 Patent format: Claim 11; Fig 52; 567pp; English.
 Comment: The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
 Database: GENESEQ patent database.

P_ABP65102 Hypoxia-induced protein #28 - Homo sapiens.
 Length: 452 aa
 Accession: P_ABP65102;
 Species: Homo sapiens.
 Keywords: Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclampsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human; patent; GENESEQ patentdb.
 Patent number: WO200246465-A2.
 Publication date: 13-JUN-2002.
 Filing date: 10-DEC-2001; 2001WO-GB05458.
 Priority: 08-DEC-2000; 2000GB-0030076. 08-FEB-2001; 2001GB-0003156.
 25-OCT-2001; 2001GB-0025666.
 Assignee: (OXFO-) OXFORD BIOMEDICA UK LTD.
 Inventors: White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA; Rayner WN;
 Cross reference: WPI; 2002-627238/67.
 Title: Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene -
 Patent format: Claim 13; Page 305; 538pp; English.
 Comment: The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological

condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

Database: GENESEQ patent database.

P_ABB99215 Human retinoid inducible serine carboxypeptidase - Homo sapiens.

Length: 452 aa

Accession: P_ABB99215;

Species: Homo sapiens.

Keywords: Serine carboxypeptidase; mammalian; RISC; antihypertensive; retinoid-inducible serine carboxypeptidase; antiarteriosclerotic; nephrotropic; antiasthmatic; vasotropic; gene therapy; vascular disease; vascular hyperplasia; atherosclerosis; restenosis; glomerulonephritis; hypertension; obstructive bladder disease; tubulosclerosis; asthma; interstitial tubular disease; human; patent; GENESEQ patentdb.

Patent number: WO200268599-A2.

Publication date: 06-SEP-2002.

Filing date: 22-FEB-2002; 2002WO-US05560.

Priority: 22-FEB-2001; 2001US-271183P. 23-MAY-2001; 2001US-293097P.

Assignee: (UYRP) UNIV ROCHESTER.

Inventors: Miano JM, Streb JW, Chen J;

Cross reference: WPI; 2002-713371/77. N-PSDB; ABV72656.

Title: New retinoid-inducible serine carboxypeptidase proteins and nucleic acids, useful for detecting or treating vascular diseases, e.g. vascular hyperplasia, atherosclerosis, asthma, glomerulonephritis, hypertension -

Patent format: Claim 39; Page 20-21; 129pp; English.

Comment: The invention relates to a novel mammalian retinoid-inducible serine carboxypeptidase (RISC) protein or polypeptide. The proteins of the invention have antiarteriosclerotic, antihypertensive, nephrotropic, antiasthmatic, and vasotropic activity. The polynucleotides of the invention may have a use in gene therapy. The retinoid-inducible serine carboxypeptidase protein and the nucleic acid molecule are useful in detecting, preventing or treating vascular diseases or disorders, e.g. vascular hyperplasia, atherosclerosis, restenosis, glomerulonephritis, hypertension, obstructive bladder disease, tubulosclerosis, asthma or interstitial tubular disease, in inhibiting smooth muscle cell growth and inhibiting the activity of extracellular regulated kinase. The transgenic animal is useful in screening and identifying agents that induce or suppress the function of the retinoid-inducible genes. The sequence represents the human RISC of

the invention.
73-82/Binding-site
/label= Serine_carboxypeptidase_binding_site/
163-170/Domain
/label= First_catalytic_domain/
365-373/Domain
/label= Second_catalytic_domain/
421-437/Domain
/label= Third_catalytic_domain/
Database: GENESEQ patent database.

P_AAB80255 Human PRO302 protein - Homo sapiens.

Length: 452 aa

Accession: P_AAB80255;

Species: Homo sapiens.

Keywords: Human; PRO; dermatological; antipsoriatic; cytostatic;
antiinflammatory; antiparkinsonian nootropic; neuroprotective;
vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic;
antirheumatic; cancer; antiarthritic; antiinfertility;
antidiabetic; antiviral; diabetes; ophthalmological; gene therapy;
skin disease; gastrointestinal disorder; ischaemia; inflammation;
patent; GENESEQ patentdb.

Patent number: WO200104311-A1.

Publication date: 18-JAN-2001.

Filing date: 22-FEB-2000; 2000WO-US04414.

Priority: 07-JUL-1999; 99US-0143048. 26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222. 08-SEP-1999; 99WO-US20594. 13-SEP-1999;
99WO-US20944. 15-SEP-1999; 99WO-US21090. 15-SEP-1999; 99WO-US21547.
05-OCT-1999; 99WO-US23089. 29-NOV-1999; 99WO-US28214. 30-NOV-1999;
99WO-US28313. 16-DEC-1999; 99WO-US30095. 20-DEC-1999; 99WO-US30911.
20-DEC-1999; 99WO-US30999. 05-JAN-2000; 99WO-US00219.

Assignee: (GETH) GENENTECH INC.

Inventors: Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ; Mather
JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood
WI;

Cross reference: WPI; 2001-081051/09. N-PSDB; AAF72416.

Title: Sixty one nucleic acids encoding PRO polypeptides which are useful
in the treatment of skin diseases (e.g. psoriasis), cancers (e.g.
lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
Alzheimer's disease) -

Patent format: Claim 1; Fig 90; 393pp; English.

Comment: The present sequence is one of sixty one novel secreted and
transmembrane PRO polypeptides. The PRO polypeptides are useful for
treating skin diseases (e.g. psoriasis), cancers (e.g. lung
squamous cell carcinoma), gastrointestinal disorders (e.g.
enterocolitis), neurodegenerative diseases (e.g. Alzheimer's
disease, Parkinson's disease), wound repair, cardiovascular
disorders (e.g. endometrial bleeding angiogenesis, ischaemias such
as coronary ischaemia, atherosclerosis), inflammatory disorders
(e.g. asthma, rheumatoid arthritis, multiple sclerosis),
infertility, AIDS and diabetes and retinal disorders such as
retinitis pigmentosum. The PRO nucleic acids have applications in
molecular biology, including use as hybridization probes, and in
chromosome and gene mapping.

Database: GENESEQ patent database.

P_AAB20341 Human PRO302 - Homo sapiens.

Length: 452 aa

Accession: P_AAB20341;

Species: Homo sapiens.

Keywords: PRO302; vitellogenic carboxypeptidase homologue; human; angiogenesis; cardiovascularisation; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; macular degeneration; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; antirheumatic; antiarthritic; antiinflammatory; vulnerary; antitumour; diagnosis; therapy; patent; GENESEQ patentdb.

Patent number: WO200119987-A1.

Publication date: 22-MAR-2001.

Filing date: 29-NOV-1999; 99WO-US28214.

Priority: 13-SEP-1999; 99WO-US20944. 15-SEP-1999; 99WO-US21090.

Assignee: (GETH) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan KJ; Williams PM, Wood WI;

Cross reference: WPI; 2001-235264/24. N-PSDB; AAF30502.

Title: Composition comprising a PRO230, PRO216 or PRO302 polypeptide, agonist or antagonist for promoting or inhibiting angiogenesis and/or cardiovascularisation in mammals -

Patent format: Claim 55; Fig 6; 141pp; English.

Comment: The present sequence is that of human PRO302, a novel secreted protein (51 kDa, pI 5.74) that is a homologue of vitellogenic carboxypeptidase. The sequence is predicted from isolated PRO302 cDNA (see AAF30502). PRO302 is 1 of 3 novel PRO polypeptides of the invention. PRO230, PRO216 and PRO302 polynucleotides and polypeptides, recombinant retroviral particles, ex vivo producer cells, expression vectors, host cells, and methods of recombinant production are provided, as well as antibodies, agonists and antagonists. The polynucleotides, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration (all claimed), atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis and lymphangitis. The polypeptides, agonists and antagonists are also used in claimed methods of stimulating or inhibiting endothelial cell growth.

1-25/Peptide

/label= Signal_peptide/

26-452/Protein

/label= Mature_protein/

64-68/Modified-site

/note= Asn is N-glycosylated/

126-130/Modified-site

/note= Asn is N-glycosylated/

362-366/Modified-site

/note= Asn is N-glycosylated/

204-208/Modified-site

/note= O-phosphorylated by casein kinase II/

220-224/Modified-site

/note= O-phosphorylated by casein kinase II/

280-284/Modified-site

/note= O-phosphorylated by casein kinase II/

284-288/Modified-site

/note= O-phosphorylated by casein kinase II/

351-355/Modified-site

/note= O-phosphorylated by casein kinase II/
449-453/Modified-site
/note= O-phosphorylated by casein kinase II/
101-105/Modified-site
/note= O-phosphorylated by cAMP- and cGMP-/
dependent protein kinase/
22-28/Modified-site
/note= N-myristoylated/
76-82/Modified-site
/note= N-myristoylated/
79-85/Modified-site
/note= N-myristoylated/
80-86/Modified-site
/note= N-myristoylated/
119-125/Modified-site
/note= N-myristoylated/
168-175/Modified-site
/note= N-myristoylated/
187-193/Modified-site
/note= N-myristoylated/
195-201/Modified-site
/note= N-myristoylated/
331-337/Modified-site
/note= N-myristoylated/
332-338/Modified-site
/note= N-myristoylated/
360-366/Modified-site
/note= N-myristoylated/
Database: GENESEQ patent database.

P_AAB93913 Human protein sequence SEQ ID NO:13882 - Homo sapiens.

Length: 452 aa

Accession: P_AAB93913;

Species: Homo sapiens.

Keywords: Human; primer; detection; diagnosis; antisense therapy; gene
therapy; patent; GENESEQ patentdb.

Patent number: EP1074617-A2.

Publication date: 07-FEB-2001.

Filing date: 28-JUL-2000; 2000EP-0116126.

Priority: 29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253.

11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767.

09-JUN-2000; 2000JP-0241899.

Assignee: (HELI-) HELIX RES INST.

Inventors: Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

Cross reference: WPI; 2001-318749/34.

Title: Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the
detection and/or diagnosis of the abnormality of the proteins
encoded by the full-length cDNAs -

Patent format: Claim 8; SEQ ID 13882; 2537pp + CD ROM; English.

Comment: The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide
complementary to the complementary strand of a polynucleotide which
comprises one of the 5602 nucleotide sequences defined in the
specification, where the oligonucleotide comprises at least 15
nucleotides; or (b) a combination of an oligonucleotide comprising

a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Database: GENESEQ patent database.

P_AAE06595 Human protein having hydrophobic domain, HP03959 - Homo sapiens.

Length: 452 aa

Accession: P_AAE06595;

Species: Homo sapiens.

Keywords: Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; patent; GENESEQ patentdb.

Patent number: WO200149728-A2.

Publication date: 12-JUL-2001.

Filing date: 28-DEC-2000; 2000WO-JP09359.

Priority: 06-JAN-2000; 2000JP-0000585. 06-JAN-2000; 2000JP-0000588.

11-JAN-2000; 2000JP-0002299. 03-FEB-2000; 2000JP-0026862.

03-MAR-2000; 2000JP-0058367.

Assignee: (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RES CENT.

Inventors: Kato S, Kimura T;

Cross reference: WPI; 2001-418355/44. N-PSDB; AAD12590.

Title: Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -

Patent format: Claim 1; Page 368-370; 563pp; English.

Comment: The present sequence is human protein with hydrophobic domain, HP03959. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate

immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.

1-27/Peptide

/label= Signal_peptide/

28-452/Protein

/note= Mature human protein with hydrophobic domain/

Database: GENESEQ patent database.

P_AAY88378 PRO302, vitellogenic carboxypeptidase homologue amino acid sequence - Homo sapiens.

Length: 452 aa

Accession: P_AAY88378;

Species: Homo sapiens.

Keywords: Human; PRO302; Vitellogenic carboxypeptidase; cardiant; angiogenic; cytostatic; ophthalmic; antiproliferative activity; cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy; trauma; cancer; myocardial infarction; age-related macular degeneration; patent; GENESEQ patentdb.

Patent number: WO200015792-A2.

Publication date: 23-MAR-2000.

Filing date: 13-SEP-1999; 99WO-US20944.

Priority: 14-SEP-1998; 98US-0100262. 14-SEP-1998; 98WO-US19177.

Assignee: (GETH) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan KJ; Williams PM, Wood WI;

Cross reference: WPI; 2000-271431/23. N-PSDB; AAA13199.

Title: A composition comprising PRO230, PRO216 or PRO302 polypeptides, agonists or antagonists useful for promotion or inhibition of cardiovascularisation, angiogenesis or endothelialisation in mammals -

Patent format: Example 3; Fig 6; 135pp; English.

Comment: This sequence represents the human PRO302 amino acid sequence.

PRO302 is a human vitellogenic carboxypeptidase homologue. The invention relates to a composition comprising a PRO230 (tubulointerstitial nephritis antigen homologue), PRO216 (osteomodulin/fibromodulin homologue) or PRO302 (vitellogenic carboxypeptidase homologue) polypeptide, or an agonist or antagonist of these. Also included in the invention is a method for preparing the composition, agonists and antagonists of PRO230, PRO216 or PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302 polypeptides. The composition of the invention has cardiant, angiogenic, cytostatic, ophthalmic, and antiproliferative activity. Analysis of the level of expression of a gene encoding a PRO230, PRO216 or PRO302 polypeptide or detecting the presence/absence of the polypeptide is useful for diagnosis of cardiovascular, endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216 or PRO302 antibodies are useful in these diagnostic methods. The PRO230, PRO216 or PRO302 polypeptides (and their coding sequences), agonists and antagonists are useful for treatment of cardiovascular, endothelial or angiogenic disorders, especially

cardiac hypertrophy (especially characterized by presence of an elevated level of PGF-2alpha), trauma or cancer, myocardial infarction or age-related macular degeneration. In particular, PRO216, an agonist of PRO216, an antagonist of PRO230, PRO216 or PR302 or an anti-PRO216 antibody is useful for inhibition of endothelial cell growth in a mammal. Endothelial cell growth can be stimulated by administration of PRO230, a PRO230 agonist or antagonist or an anti-PRO230 antibody. Additionally, an anti-PRO302 antibody can inhibit angiogenesis induced by PRO302 in a mammal.

Database: GENESEQ patent database.

P_AAY13387 Amino acid sequence of protein PRO302 - Homo sapiens.

Length: 452 aa

Accession: P_AAY13387;

Species: Homo sapiens.

Keywords: Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; patent; GENESEQ patentdb.

Patent number: WO9914328-A2.

Publication date: 25-MAR-1999.

Filing date: 16-SEP-1998; 98WO-US19330.

Priority: 25-NOV-1997; 97US-0066840. 17-SEP-1997; 97US-0059113.

17-SEP-1997; 97US-0059115.24-NOV-1997; 97US-0066511. 24-NOV-1997;

97US-0066453. plus 47 more dates.

Assignee: (GETH) GENENTECH INC.

Inventors: Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

Cross reference: WPI; 1999-229533/19. N-PSDB; AAX52258.

Title: New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

Patent format: Claim 12; Fig 90; 320pp; English.

Comment: AAY13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

Database: GENESEQ patent database.

P_AAY05768 Human PRO216 (vitellogenic carboxypeptidase homologue) - Homo sapiens.

Length: 452 aa

Accession: P_AAY05768;

Species: Homo sapiens.

Keywords: PRO302; vitellogenic carboxypeptidase; human; angiogenesis; cardiovascularisation; wound healing; cancer; atherosclerosis; cardiac hypertrophy; myocardial infarction; antiangiogenic; antitumour; tissue regeneration; pulmonary fibrosis; neurological disease; macular degeneration; diagnosis; therapy; patent; GENESEQ patentdb.

Patent number: WO9914234-A2.

Publication date: 25-MAR-1999.

Filing date: 14-SEP-1998; 98WO-US19177.

Priority: 24-NOV-1997; 97US-0066772. 17-SEP-1997; 97US-0059117.

27-OCT-1997; 97US-0063329.

Assignee: (GETH) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan K; Williams PM, Woodwi;

Cross reference: WPI; 1999-254381/21. N-PSDB; AAX25445.

Title: Composition containing human polypeptides with anti-angiogenic activity

Patent format: Example 1; Fig 9; 102pp; English.

Comment: The present sequence represents human PRO302, identified as a vitellogenic carboxypeptidase homologue. The sequence was deduced from cDNA clone UNQ265 (DNA40370-1217, ATCC 209485, see AAX25445). Compositions containing PRO302, PRO216 (human osteomodulin, see AAY05767) or PRO230 in admixture with a carrier are claimed. The compositions are used to treat or prevent a wide range of cardiovascular, endothelial and angiogenic disorders (claimed), specifically cardiac hypertrophy (especially where associated with elevated levels of prostaglandin F2 alpha or induced by myocardial infarction), trauma (wounds, burns, or tissue regeneration more generally, including neurological disease), and cancer. Antagonists may be used similarly, also to treat age-related macular degeneration (or other angiogenic retinal disorders) and to prevent excessive growth of connective tissue during wound healing or in pulmonary fibrosis.

1-25/Peptide

/note= signal peptide/

26-452/Protein

/note= mature protein/

64/Modified-site

/note= N-glycosylated/

126/Modified-site

/note= N-glycosylated/

362/Modified-site

/note= N-glycosylated/

Database: GENESEQ patent database.

CAC51169.1 unnamed protein product - Homo sapiens

Length: 452 aa

Species: Homo sapiens (human)

Kato, S. and Kimura, T., Patent: WO 0149728-A 85 12-JUL-2001; Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP) Title: Human proteins having hydrophobic domains and dnas encoding these proteins

Locus: AX191563
Accession: AX191563
Cross-references: taxon:9606; GI:15209750; AX191563_1
Database: GBTRANS

AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens
Length: 452 aa
Species: Homo sapiens (human)
Cho, J.-J. and Baik, H.-H., Submitted (26-JUN-2000) Microbiology, Kyung Hee University, Hoeki 1, Seoul 130-701, Korea Title: Direct Submission
Gene: HSCP1
Locus: AF282618
Accession: AF282618
Cross-references: taxon:9606; GI:10312169; AF282618_1
Database: GBTRANS

BAB55069.1 unnamed protein product - Homo sapiens
Length: 452 aa
Species: Homo sapiens (human)
Isogai, T. and Otsuki, T., Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) Title: Direct Submission
Locus: AK027373
Accession: AK027373
Cross-references: taxon:9606; GI:14042006; AK027373_1
Database: GBTRANS

RISC_HUMAN Retinoid-inducible serine carboxypeptidase precursor
/pid=AAG16692.1 - homo sapiens
Length: 452 aa
Species: Homo sapiens (Human).
Accession: Q9HB40; EMBL; AF282618; AAG16692.1. EMBL; AK027373; BAB55069.1. MEROPS; S10.013; -. InterPro; IPR000379; Ser_estrs_site. InterPro; IPR001563; Serine_carbpept. Pfam; PF00450; serine_carbpept; 1. PRINTS; PR00724; CRBOXYPTASEC. ProDom; PD001189; Serine_carbpept; 2. PROSITE; PS00131; CARBOXYPEPT_SER_SER; 1. PROSITE; PS00560; CARBOXYPEPT_SER_HIS; FALSE_NEG.
Cho J.-J., Baik H.-H., Submitted (jun-2000) to the Embl/genbank/ddbj databases. (ref. 1: sequence from n.a.) Title: "Cloning of novel serine carboxypeptidase precursor."
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Submitted (may-2001) to the Embl/genbank/ddbj databases. (ref. 2: sequence from n.a. tissue=mammary gland;) Title: "NEDO human cDNA sequencing project."
Keywords: hydrolase; carboxypeptidase; glycoprotein; signal.
Taxid: tx:9606
Gene name: RISC OR SCP1.
1-26/Domain: Signal Potential.
27-452/Domain: Retinoid-Inducible Serine Carboxypeptidase.
167/Site: Act_site By Similarity.
371/Site: Act_site By Similarity.
431/Site: Act_site By Similarity.

64/Site: Carbohyd N-Linked (glcnac...) (potential).
126/Site: Carbohyd N-Linked (glcnac...) (potential).
362/Site: Carbohyd N-Linked (glcnac...) (potential).
Database: Swissprot (SPROT), Release 40 (Jan 11, 2003)

P_AAU96225 Human secreted protein, SEQ ID No 127 - Homo sapiens.

Length: 452 aa

Accession: P_AAU96225;

Species: Homo sapiens.

Keywords: Human; secreted protein; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast; liver; ischaemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; corneal infection; wound healing; ocular disorder; skin aging; sunburn; epithelial cell proliferation; organ transplantation; food additive; food storage; patent; GENESEQ patentdb.

Patent number: WO200224721-A1.

Publication date: 28-MAR-2002.

Filing date: 09-JAN-2001; 2001WO-US00544.

Priority: 20-SEP-2000; 2000US-234211P.

Assignee: (HUMA-) HUMAN GENOME SCI INC.

Inventors: Komatsoulis GA, Baker KP, Rosen CA, Birse CE, Soppet DR, Olsen HS; Ni J, Fiscella M, Moore PA, Wei P, Ebner R, Duan DR, Shi Y; Choi GH;

Cross reference: WPI; 2002-330012/36.

Title: Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

Patent format: Disclosure; Page 13; 562pp; English.

Comment: The invention relates to an isolated nucleic acid molecule (I) encoding a human secreted protein (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to (II) can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAU96165-AAU96237 represent human secreted protein sequences and related sequences used in expression of the secreted proteins as described in examples of the invention.

Database: GENESEQ patent database.

P_AAB41675 Human ORFX ORF1439 polypeptide sequence SEQ ID NO:2878 - Homo sapiens.

Length: 451 aa

Accession: P_AAB41675;

Species: Homo sapiens.

Keywords: Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; patent; GENESEQ patentdb.

Patent number: WO200058473-A2.

Publication date: 05-OCT-2000.

Filing date: 31-MAR-2000; 2000WO-US08621.

Priority: 31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

Assignee: (CURA-) CURAGEN CORP.

Inventors: Shimkets RA, Leach M;

Cross reference: WPI; 2000-602362/57. N-PSDB; AAC75884.

Title: Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Patent format: Claim 11; Page 2115-2116; 5507pp; English.

Comment: AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

Database: GENESEQ patent database.

AAG39285.1 MSTP034 - Homo sapiens

Length: 402 aa

Species: Homo sapiens (human)

Liu,B., Liu,Y.Q., Wang,X.Y., Zhao,B., Sheng,H., Zhao,X.W., Liu,S., Xu,Y.Y.,
Ye,J., Song,L., Gao,Y., Zhang,C.L., Zhang,J., Wei,Y.J., Cao,H.Q.,
Zhao,Y., Liu,L.S., Ding,J.F., Gao,R.L., Wu,Q.Y., Qiang,B.Q.,
Yuan,J.G., Liew,C.C., Zhao,M.S. and Hui,R.T., Submitted
(15-DEC-1998) Molecular Medical Center for Cardiovascular Disease,
Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing
100037, P.R. China Title: Direct Submission

Locus: AF113214

Accession: AF113214

Cross-references: taxon:9606; GI:11640576; AF113214_1

Database: GBTRANS



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Tue Apr 1 15:57:45 2003 [BLAST 2.2 [Jan-08-2002], NCBI]
Repeats masked (summary below)
/home/glinda/vf/Legal/byeung/ss.DNA40370 (1650 bp)

Sequences producing High-scoring Segment Pairs:		Frame	Score	Match	Pct	E-val
1	P_AAF30502 Human PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
2	P_AAA13199 PRO302, vitellogenic carboxypeptidase h	+	1650	1650	100	0.0
3	P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217	+	1650	1650	100	0.0
4	P_AAX25445 Human PRO216 cDNA clone UNQ265.	+	1650	1650	100	0.0
5	P_AAF72416 Human PRO302 cDNA.	+	1650	1650	100	0.0
6	P_ABL95586 Human angiogenesis related cDNA PRO302	+	1650	1650	100	0.0
7	P_ABL88097 Human PRO302 cDNA sequence SEQ ID NO:51	+	1650	1650	100	0.0
8	AX098272 Sequence 11 from Patent WO0119987. DNA	+	1650	1650	100	0.0
9	AX454466 Sequence 51 from Patent WO0208284. DNA	+	1650	1650	100	0.0
10	BD075577 Secretory and transmembrane polypeptide	+	1650	1650	100	0.0
11	BD173394 Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
12	BD173075 Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
13	AX490944 Sequence 51 from Patent WO0200690. DNA	+	1650	1650	100	0.0
14	BD172756 Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
15	BD172437 Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
16	BD175428 Secretory and transmembrane polypeptide	+	1650	1650	100	0.0
17	P_ABV72656 Human retinoid inducible serine carboxy	+	1648	1648	100	0.0
18	P_ABV77921 Hypoxia-induced protein coding sequence	+	1640	1646	100	0.0
19	AF282618 Homo sapiens serine carboxypeptidase 1	+	1640	1646	100	0.0
20	NM_021626 Homo sapiens likely homolog of rat and	+	1640	1646	100	0.0
21	P_AAH15579 Human cDNA sequence SEQ ID NO:13881.	+	1637	1640	100	0.0
22	P_ABV28721 Human prostate expression marker cDNA 2	+	1637	1637	100	0.0
23	AK027373 Homo sapiens cDNA FLJ14467 fis, clone M	+	1637	1640	100	0.0
24	BD157571 Primer for synthesizing full-length cDN	+	1637	1640	100	0.0
25	P_AAH72787 Human cervical cancer marker nucleic ac	+	1633	1633	100	0.0
26	AX188369 Sequence 4064 from Patent WO0142467. D	+	1633	1633	100	0.0
27	P_AAD12590 Human protein having hydrophobic domain	+	1619	1622	100	0.0
28	AX191563 Sequence 85 from Patent WO0149728. DNA	+	1619	1622	100	0.0
29	AF113214 Homo sapiens MSTP034 mRNA, complete cds	+	1594	1594	100	0.0
30	P_AAC75884 Human ORFX ORF1439 polynucleotide seque	+	1543	1619	99	0.0
31	P_ABK30363 Human G-protein-coupled protease #133.	+	1407	1620	98	0.0
32	P_AAH89926 Human bone marrow cDNA, SEQ ID NO: 57.	+	1389	1577	97	0.0
33	AX191553 Sequence 75 from Patent WO0149728. DNA	+	1355	1358	100	0.0

>1 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. cDNA, PAT 29-MAY-2001
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
P_AAF30502      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
P_AAF30502     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370    121 GACTGGCCACACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAF30502    121 GACTGGCCACACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370    181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****
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P_AAF30502 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

P_AAF30502 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC

P_AAF30502 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

P_AAF30502 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

P_AAF30502 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

P_AAF30502 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC

P_AAF30502 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTTCGGTG

P_AAF30502 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

P_AAF30502 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

P_AAF30502 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

P_AAF30502 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370 841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

P_AAF30502 841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370 901 CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

P_AAF30502 901 CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

P_AAF30502 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAF30502 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

P_AAF30502	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA

P_AAF30502	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

P_AAF30502	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

P_AAF30502	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

P_AAF30502	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

P_AAF30502	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

P_AAF30502	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

P_AAF30502	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

P_AAF30502	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA

P_AAF30502	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>2 P_AAA13199 PRO302, vitellogenic carboxypeptidase homologue nucleotide sequence. (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

P_AAA13199	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

P_AAA13199	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

P_AAA13199	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

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*****
P_AAA13199      181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTGGCC
ss.DNA40370     241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
*****
P_AAA13199      241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370     301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
*****
P_AAA13199      301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
ss.DNA40370     361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
*****
P_AAA13199      361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370     421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
*****
P_AAA13199      421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370     481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
*****
P_AAA13199      481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370     541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
*****
P_AAA13199      541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370     601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTCCGGTG
*****
P_AAA13199      601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370     661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
P_AAA13199      661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370     721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
P_AAA13199      721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370     781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
*****
P_AAA13199      781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370     841 TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
P_AAA13199      841 TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370     901 CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
P_AAA13199      901 CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
P_AAA13199      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
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P_AAA13199      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

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ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

P_AAA13199	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

P_AAA13199	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

P_AAA13199	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

P_AAA13199	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

P_AAA13199	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

P_AAA13199	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

P_AAA13199	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

P_AAA13199	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

P_AAA13199	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA

P_AAA13199	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>3 P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. DNA, PAT 25-JUN-1999
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

P_AAX52258	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

P_AAX52258	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

P_AAX52258	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

P_AAX52258	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

P_AAX52258	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC

P_AAX52258	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

P_AAX52258	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

P_AAX52258	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

P_AAX52258	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC

P_AAX52258	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG

P_AAX52258	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

P_AAX52258	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

P_AAX52258	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

P_AAX52258	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACATAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

P_AAX52258	841	TATAACATCTTAACATAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

P_AAX52258	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

P_AAX52258	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAX52258	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAX52258	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA *****
P_AAX52258	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
P_AAX52258	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAX52258	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAX52258	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
P_AAX52258	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAX52258	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAX52258	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG *****
P_AAX52258	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAX52258	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>4 P_AAX25445 Human PRO216 cDNA clone UNQ265. (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_AAX25445	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_AAX25445	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_AAX25445	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAX25445	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
P_AAX25445	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
P_AAX25445	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
P_AAX25445	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX25445	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAX25445	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCA GCGAGGGACCATC
P_AAX25445	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCA GCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTCCGGTG
P_AAX25445	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX25445	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX25445	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
P_AAX25445	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX25445	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX25445	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX25445	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAX25445 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

P_AAX25445 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

P_AAX25445 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370 1201 GAACTGCCTAAATTCAAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

P_AAX25445 1201 GAACTGCCTAAATTCAAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

P_AAX25445 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370 1321 GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

P_AAX25445 1321 GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

P_AAX25445 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

P_AAX25445 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

P_AAX25445 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

P_AAX25445 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

ss.DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA

P_AAX25445 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>5 P_AAF72416 Human PRO302 cDNA. (1650 bp)/ [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

P_AAF72416 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

P_AAF72416 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

P_AAF72416 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

P_AAF72416	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

P_AAF72416	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC

P_AAF72416	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

P_AAF72416	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

P_AAF72416	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

P_AAF72416	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC

P_AAF72416	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG

P_AAF72416	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

P_AAF72416	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

P_AAF72416	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTC

P_AAF72416	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTC
ss.DNA40370	841	TATAACATCTTAACATAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

P_AAF72416	841	TATAACATCTTAACATAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

P_AAF72416	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

P_AAF72416	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAF72416	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAF72416	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
P_AAF72416	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG *****
P_AAF72416	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAF72416	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAF72416	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
P_AAF72416	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAF72416	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAF72416	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
P_AAF72416	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAF72416	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>6 P_ABL95586 Human angiogenesis related cDNA PRO302 SEQ ID NO: 51. (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_ABL95586	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_ABL95586	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_ABL95586	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

P_ABL95586	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG

P_ABL95586	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC

P_ABL95586	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTTCAGTTATGTGAATGGTAGTGGT

P_ABL95586	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

P_ABL95586	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

P_ABL95586	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC

P_ABL95586	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTCGGTG

P_ABL95586	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

P_ABL95586	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

P_ABL95586	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

P_ABL95586	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

P_ABL95586	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

P_ABL95586	901	CAGAGCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

P_ABL95586	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

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P_ABL95586      1021 TGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
P_ABL95586      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370     1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
P_ABL95586      1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370     1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
P_ABL95586      1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
P_ABL95586      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370     1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
P_ABL95586      1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
P_ABL95586      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
P_ABL95586      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
P_ABL95586      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
P_ABL95586      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370     1621 ATCAAATAAAGGATGATAATAGATATTAA
*****
P_ABL95586      1621 ATCAAATAAAGGATGATAATAGATATTAA

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>7 P_ABL88097 Human PRO302 cDNA sequence SEQ ID NO:51. cDNA, PAT 16-MAY-2002
(1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370     1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
P_ABL88097      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
P_ABL88097      61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370     121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****

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P_ABL88097 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
 ss.DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

 P_ABL88097 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
 ss.DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG

 P_ABL88097 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG
 ss.DNA40370 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCC

 P_ABL88097 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCC
 ss.DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT

 P_ABL88097 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
 ss.DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

 P_ABL88097 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
 ss.DNA40370 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

 P_ABL88097 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
 ss.DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC

 P_ABL88097 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
 ss.DNA40370 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCGTGTTGATTGCGGTG

 P_ABL88097 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCGTGTTGATTGCGGTG
 ss.DNA40370 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

 P_ABL88097 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
 ss.DNA40370 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

 P_ABL88097 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
 ss.DNA40370 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC

 P_ABL88097 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
 ss.DNA40370 841 TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA

 P_ABL88097 841 TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA
 ss.DNA40370 901 CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

 P_ABL88097 901 CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
 ss.DNA40370 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

 P_ABL88097 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_ABL88097	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

P_ABL88097	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

P_ABL88097	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

P_ABL88097	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

P_ABL88097	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

P_ABL88097	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

P_ABL88097	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

P_ABL88097	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

P_ABL88097	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTG

P_ABL88097	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA

P_ABL88097	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>8 AX098272 Sequence 11 from Patent WO0119987. DNA, linear, PAT 02-APR-2001
 (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

AX098272	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

AX098272	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

AX098272	121	***** GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC *****
AX098272	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG *****
AX098272	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC *****
AX098272	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT *****
AX098272	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
AX098272	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA *****
AX098272	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC *****
AX098272	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCCGGTG *****
AX098272	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
AX098272	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
AX098272	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC *****
AX098272	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
AX098272	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
AX098272	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC *****
AX098272	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC

ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

AX098272	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

AX098272	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA

AX098272	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCACTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

AX098272	1201	GAACTGCCTAAATTCACTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

AX098272	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

AX098272	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

AX098272	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

AX098272	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

AX098272	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

AX098272	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA

AX098272	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>9 AX454466 Sequence 51 from Patent WO0208284. DNA, linear, PAT 06-JUL-2002
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

AX454466	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

AX454466	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

AX454466	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

AX454466	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

AX454466	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC

AX454466	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

AX454466	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

AX454466	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

AX454466	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC

AX454466	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGGTG

AX454466	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

AX454466	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

AX454466	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

AX454466	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

AX454466	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

AX454466	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

AX454466	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX454466	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX454466	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
AX454466	1141	CTGGATCTCATCGTAGATACCATGGGTCTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX454466	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
AX454466	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX454466	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX454466	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX454466	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
AX454466	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
AX454466	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
AX454466	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>10 BD075577 Secretory and transmembrane polypeptide and nucleic acid encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
BD075577	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
BD075577	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

BD075577	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

BD075577	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

BD075577	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC

BD075577	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT

BD075577	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

BD075577	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCACTTGCCACAAAGAATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

BD075577	481	TTCACTTGCCACAAAGAATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC

BD075577	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCCGGTG

BD075577	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

BD075577	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

BD075577	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTC

BD075577	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

BD075577	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA

BD075577	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAAGAGCTCAAAATTATTCCTGAGGATCAATCC

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*****
BD075577      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370   1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD075577      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370   1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD075577      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370   1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAACTGAAGTGGCCA
*****
BD075577      1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370   1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG
*****
BD075577      1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG
ss.DNA40370   1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD075577      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370   1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD075577      1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370   1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD075577      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370   1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD075577      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370   1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD075577      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370   1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
*****
BD075577      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
ss.DNA40370   1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD075577      1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>11 BD173394 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370   1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
BD173394      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370   61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****

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BD173394	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

BD173394	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

BD173394	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

BD173394	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCC

BD173394	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

BD173394	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

BD173394	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCACTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

BD173394	481	TTCACTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC

BD173394	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGGTG

BD173394	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

BD173394	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

BD173394	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

BD173394	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

BD173394	841	TATAACATCTTAACTAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

BD173394	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

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ss.DNA40370  961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
BD173394     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370  1021 TGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD173394     1021 TGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370  1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD173394     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370  1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
BD173394     1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370  1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD173394     1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370  1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD173394     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370  1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD173394     1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370  1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD173394     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370  1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD173394     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370  1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD173394     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370  1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
*****
BD173394     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG

ss.DNA40370  1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD173394     1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>12 BD173075 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370  1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
BD173075     1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370  61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

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BD173075	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

BD173075	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

BD173075	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

BD173075	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCC

BD173075	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT

BD173075	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

BD173075	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

BD173075	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC

BD173075	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGTG

BD173075	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTTCTCTGAAGACAAAGGTCTGGCAGAG

BD173075	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTTCTCTGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

BD173075	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC

BD173075	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

BD173075	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

BD173075	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

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ss.DNA40370   961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
BD173075     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370   1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD173075     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370   1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD173075     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370   1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
BD173075     1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370   1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD173075     1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370   1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD173075     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370   1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD173075     1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370   1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTGGGGGCACAGAGCT
*****
BD173075     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTGGGGGCACAGAGCT

ss.DNA40370   1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD173075     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370   1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD173075     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370   1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTG
*****
BD173075     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTG

ss.DNA40370   1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD173075     1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>13 AX490944 Sequence 51 from Patent WO0200690. DNA, linear, PAT 16-AUG-2002
(1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370   1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
AX490944      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

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ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

AX490944	61	GTCCCGCGGTGGTTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCAACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

AX490944	121	GACTGGCCCAACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTCCCC

AX490944	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTCCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

AX490944	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC

AX490944	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAAGTTATGTGAATGGTAGTGGT

AX490944	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

AX490944	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA

AX490944	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC

AX490944	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCTGGATCTCCCTGTTGATTCCGGTG

AX490944	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCTGGATCTCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

AX490944	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

AX490944	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC

AX490944	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

AX490944	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

AX490944	901	CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
AX490944	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX490944	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX490944	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA *****
AX490944	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGGAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX490944	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGGAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTGCTTTCTACTGGATTCTGAAAGCT *****
AX490944	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX490944	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX490944	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX490944	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
AX490944	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
AX490944	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
AX490944	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>14 BD172756 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
BD172756	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

 BD172756 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

 BD172756 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

 BD172756 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

ss.DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

 BD172756 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG

ss.DNA40370 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

 BD172756 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

ss.DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

 BD172756 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT

ss.DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

 BD172756 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

ss.DNA40370 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

 BD172756 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA

ss.DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC

 BD172756 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC

ss.DNA40370 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG

 BD172756 601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG

ss.DNA40370 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

 BD172756 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG

ss.DNA40370 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

 BD172756 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC

ss.DNA40370 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC

 BD172756 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC

ss.DNA40370 841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

 BD172756 841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

ss.DNA40370 901 CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

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BD172756 901 CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTCTGAGGATCAATCC
*****
BD172756 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTCTGAGGATCAATCC
ss.DNA40370 1021 TGGGGAGGCCAGGCTACCAACGCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD172756 1021 TGGGGAGGCCAGGCTACCAACGCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD172756 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTCTAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
*****
BD172756 1141 CTGGATCTCATCGTAGATACCATGGGTCTAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD172756 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD172756 1261 GAAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370 1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD172756 1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGCGGCACAGAGCT
*****
BD172756 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGCGGCACAGAGCT
ss.DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD172756 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD172756 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
*****
BD172756 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTG
ss.DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD172756 1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>15 BD172437 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****

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BD172437	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
BD172437	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCAAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
BD172437	121	GACTGGCCCAAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC *****
BD172437	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG *****
BD172437	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC *****
BD172437	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT *****
BD172437	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
BD172437	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA *****
BD172437	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC *****
BD172437	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCGGTG *****
BD172437	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
BD172437	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
BD172437	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC *****
BD172437	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
BD172437	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

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ss.DNA40370   901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
BD172437      901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

ss.DNA40370   961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
*****
BD172437      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC

ss.DNA40370   1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD172437      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370   1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD172437      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370   1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
BD172437      1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370   1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD172437      1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370   1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD172437      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370   1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD172437      1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370   1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD172437      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370   1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD172437      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370   1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD172437      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370   1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTG
*****
BD172437      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTG

ss.DNA40370   1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD172437      1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>16 BD175428 Secretory and transmembrane polypeptide and nucleic acid encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370   1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

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*****
BD175428      1  GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370   61  GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
BD175428      61  GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370   121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
BD175428      121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370   181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****
BD175428      181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370   241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
*****
BD175428      241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370   301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
*****
BD175428      301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370   361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
*****
BD175428      361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370   421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
*****
BD175428      421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370   481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
*****
BD175428      481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370   541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
*****
BD175428      541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
ss.DNA40370   601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGGTG
*****
BD175428      601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370   661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
BD175428      661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370   721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
BD175428      721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370   781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
*****
BD175428      781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370   841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
BD175428      841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

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ss.DNA40370  901 CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
                *****
BD175428     901 CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

ss.DNA40370  961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
                *****
BD175428     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC

ss.DNA40370  1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
                *****
BD175428     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370  1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
                *****
BD175428     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370  1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
                *****
BD175428     1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA

ss.DNA40370  1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
                *****
BD175428     1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370  1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
                *****
BD175428     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370  1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
                *****
BD175428     1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370  1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
                *****
BD175428     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370  1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
                *****
BD175428     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370  1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
                *****
BD175428     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370  1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTG
                *****
BD175428     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTG

ss.DNA40370  1621 ATCAAAATAAAGGATGATAATAGATATTAA
                *****
BD175428     1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>17 P_ABV72656 Human retinoid inducible serine carboxypeptidase cDNA. (1921 bp)
[1 seg]

Score = 1648 (3267 bits), Expect = 0.0

Identities = 1648/1648 (100%), at 2,1-1649,1648, Strand +/-

ss.DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGGTACTTGT	CATGGAGCTGGCACTGCGGCGCTCTCCCCG

P_ABV72656	1	CCTGTTGCTGATGCTGCCGTGCGGTACTTGT	CATGGAGCTGGCACTGCGGCGCTCTCCCCG
ss.DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCT	GCTGGGCCTGAACGCAGGAGCTGTCATTG

P_ABV72656	61	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCT	GCTGGGCCTGAACGCAGGAGCTGTCATTG
ss.DNA40370	122	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGG	ATTATGTGACGGTCCGCAAGGATGCCT

P_ABV72656	121	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGG	ATTATGTGACGGTCCGCAAGGATGCCT
ss.DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACT	CCTGCAAGAACTTCTCAGAACTGCCCC

P_ABV72656	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACT	CCTGCAAGAACTTCTCAGAACTGCCCC
ss.DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTT	CTAGCACTGGATTGGAACCTTTGAGG

P_ABV72656	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTT	CTAGCACTGGATTGGAACCTTTGAGG
ss.DNA40370	302	AAATTGGGCCCCCTTGACAGTGATCTCAAACCA	CGGAAAACCACCTGGCTCCAGGCTGCCA

P_ABV72656	301	AAATTGGGCCCCCTTGACAGTGATCTCAAACCA	CGGAAAACCACCTGGCTCCAGGCTGCCA
ss.DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACT	GGGTTTCAGTTATGTGAATGGTAGTGGTG

P_ABV72656	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACT	GGGTTTCAGTTATGTGAATGGTAGTGGTG
ss.DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAG	ACATGATGGTTCTCCTGAAGACCTTCT

P_ABV72656	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAG	ACATGATGGTTCTCCTGAAGACCTTCT
ss.DNA40370	482	TCAGTTGCCACAAAGAATTCAGACAGTTCCATT	TCTACATTTTCTCAGAGTCTTATGGAG

P_ABV72656	481	TCAGTTGCCACAAAGAATTCAGACAGTTCCATT	TCTACATTTTCTCAGAGTCTTATGGAG
ss.DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTT	TATAAGGCCATTACGCGAGGGACCATCA

P_ABV72656	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTT	TATAAGGCCATTACGCGAGGGACCATCA
ss.DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCCTGGGTGATT	CCTGGATCTCCCCTGTTGATTCCGTGC

P_ABV72656	601	AGTGCAACTTTGCGGGGGTTGCCCTGGGTGATT	CCTGGATCTCCCCTGTTGATTCCGTGC
ss.DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTC	TTCTCGAAGACAAAGGTCTGGCAGAGG

P_ABV72656	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTC	TTCTCGAAGACAAAGGTCTGGCAGAGG
ss.DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCG	TAAATAAGGGGCTCTACAGAGAGGCCA

P_ABV72656	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCG	TAAATAAGGGGCTCTACAGAGAGGCCA
ss.DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATT	GAAACAGAACACAGATGGGGTGAACCTCT

P_ABV72656	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATT	GAAACAGAACACAGATGGGGTGAACCTCT
ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCT	ACAATGGAGTCGAGTCTAGAATTCACAC

P_ABV72656	841	ATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

P_ABV72656	901	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT

P_ABV72656	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
ss.DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

P_ABV72656	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC

P_ABV72656	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG

P_ABV72656	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
ss.DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

P_ABV72656	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG

P_ABV72656	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370	1322	GTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

P_ABV72656	1321	GTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

P_ABV72656	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG

P_ABV72656	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
ss.DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

P_ABV72656	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA

P_ABV72656	1561	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
ss.DNA40370	1622	TCAAAATAAAGGATGATAATAGATATTA

P_ABV72656	1621	TCAAAATAAAGGATGATAATAGATATTA

>18 P_ABV77921 Hypoxia-induced protein coding sequence #35. DNA, PAT 12-NOV-2002 (1921 bp) [1 seg]

Score = 1640 (3251 bits), Expect = 0.0

Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

ss.DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG

P_ABV77921	1	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
ss.DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTG

P_ABV77921	61	TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTG
ss.DNA40370	122	ACTGGCCCAACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT

P_ABV77921	121	ACTGGCCCAACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
ss.DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC

P_ABV77921	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
ss.DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGG

P_ABV77921	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAGG
ss.DNA40370	302	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCCA

P_ABV77921	301	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCCA
ss.DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAATTATGTGAATGGTAGTGGTG

P_ABV77921	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAATTATGTGAATGGTAGTGGTG
ss.DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT

P_ABV77921	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
ss.DNA40370	482	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG

P_ABV77921	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
ss.DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA

P_ABV77921	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
ss.DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTCCGGTGC

P_ABV77921	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTCCGGTGC
ss.DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG

P_ABV77921	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
ss.DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA

P_ABV77921	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
ss.DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT

P_ABV77921	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT
ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC

```

*****
P_ABV77921      841 ATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370     902 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
*****
P_ABV77921      901 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370     962 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTGAGGATCAATCCT
*****
P_ABV77921      961 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTGAGGATCAATCCT
ss.DNA40370     1022 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
*****
P_ABV77921      1021 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370     1082 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
*****
P_ABV77921      1081 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370     1142 TGGATCTCATCGTAGATACCATGGGTCTAGGAGGCCCTGGGTGCGGAACTGAAGTGGCCAG
*****
P_ABV77921      1141 TGGATCTCATCGTAGATACCATGGGTCTAGGAGGCCCTGGGTGCGGAACTGAAGTGGCCAG
ss.DNA40370     1202 AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
*****
P_ABV77921      1201 AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370     1262 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG
*****
P_ABV77921      1261 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370     1322 GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
*****
P_ABV77921      1321 GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370     1382 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
*****
P_ABV77921      1381 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370     1442 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
*****
P_ABV77921      1441 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
ss.DNA40370     1502 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
*****
P_ABV77921      1501 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370     1562 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA
*****
P_ABV77921      1561 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA
ss.DNA40370     1622 TCAAAATAAAGGATGATAATAGATATTA
*****
P_ABV77921      1621 TCAAAATAAAGGATGATAATAGATATTA

```

>19 AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
(1921 bp) [1 seg]
Score = 1640 (3251 bits), Expect = 0.0

Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

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ss.DNA40370      2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
AF282618         1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG

ss.DNA40370      62 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
AF282618         61 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG

ss.DNA40370      122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
AF282618         121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT

ss.DNA40370      182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
AF282618         181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC

ss.DNA40370      242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
*****
AF282618         241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG

ss.DNA40370      302 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA
*****
AF282618         301 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA

ss.DNA40370      362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTG
*****
AF282618         361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTG

ss.DNA40370      422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
*****
AF282618         421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT

ss.DNA40370      482 TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
*****
AF282618         481 TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG

ss.DNA40370      542 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCA
*****
AF282618         541 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCA

ss.DNA40370      602 AGTGCAACTTTGCGGGGGTTGCC/TTGGGTGATTCTCGGATCTCCCCGTGTTGATTGCGGTGC
*****
AF282618         601 AGTGCAACTTTGCGGGGGTTGCC/TTGGGTGATTCTCGGATCTCCCCGTGTTGATTGCGGTGC

ss.DNA40370      662 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
*****
AF282618         661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG

ss.DNA40370      722 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
*****
AF282618         721 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA

ss.DNA40370      782 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
*****
AF282618         781 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
```

ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC

AF282618	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

AF282618	901	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCT

AF282618	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCT
ss.DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

AF282618	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC

AF282618	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCAG

AF282618	1141	TGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCAG
ss.DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

AF282618	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG

AF282618	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

AF282618	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

AF282618	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCTGTATCTAACTGGGGCTGTG

AF282618	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCTGTATCTAACTGGGGCTGTG
ss.DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

AF282618	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA

AF282618	1561	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
ss.DNA40370	1622	TCAAATAAAGGATGATAATAGATATTA

AF282618	1621	TCAAATAAAGGATGATAATAGATATTA

>20 NM_021626 Homo sapiens likely homolog of rat and mouse retinoid-inducible (1921 bp) [1 seg]

Score = 1640 (3251 bits), Expect = 0.0
Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

```
ss.DNA40370      2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
   NM_021626      1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG

ss.DNA40370     62 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
   NM_021626     61 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG

ss.DNA40370    122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
   NM_021626    121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT

ss.DNA40370    182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
   NM_021626    181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC

ss.DNA40370    242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGCTTTGAGG
   NM_021626    241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGCTTTGAGG

ss.DNA40370    302 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAACACCTGGCTCCAGGCTGCCA
   NM_021626    301 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGGAACACCTGGCTCCAGGCTGCCA

ss.DNA40370    362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTG
   NM_021626    361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTG

ss.DNA40370    422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
   NM_021626    421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT

ss.DNA40370    482 TCAGTTGCCACAAAGAATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
   NM_021626    481 TCAGTTGCCACAAAGAATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG

ss.DNA40370    542 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
   NM_021626    541 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA

ss.DNA40370    602 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCGTGTTGATTGCGGTGC
   NM_021626    601 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCGTGTTGATTGCGGTGC

ss.DNA40370    662 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
   NM_021626    661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG

ss.DNA40370    722 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
   NM_021626    721 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA

ss.DNA40370    782 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
   NM_021626    781 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
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ss.DNA40370 842 ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC

 NM_021626 841 ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC

ss.DNA40370 902 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

 NM_021626 901 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA

ss.DNA40370 962 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCCT

 NM_021626 961 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCCT

ss.DNA40370 1022 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

 NM_021626 1021 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA

ss.DNA40370 1082 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGATAATGGACAGC

 NM_021626 1081 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGATAATGGACAGC

ss.DNA40370 1142 TGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCAG

 NM_021626 1141 TGGATCTCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCAG

ss.DNA40370 1202 AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

 NM_021626 1201 AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG

ss.DNA40370 1262 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG

 NM_021626 1261 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG

ss.DNA40370 1322 GTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

 NM_021626 1321 GTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC

ss.DNA40370 1382 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

 NM_021626 1381 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG

ss.DNA40370 1442 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG

 NM_021626 1441 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG

ss.DNA40370 1502 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

 NM_021626 1501 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT

ss.DNA40370 1562 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA

 NM_021626 1561 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA

ss.DNA40370 1622 TCAAAATAAAGGATGATAATAGATATTA

 NM_021626 1621 TCAAAATAAAGGATGATAATAGATATTA

Score = 1637 (3245 bits), Expect = 0.0
Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/+

```
ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
*****
P_AAH15579      1 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
*****
P_AAH15579     61 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCACATGT
*****
P_AAH15579    121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA
*****
P_AAH15579    181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
*****
P_AAH15579    241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG

ss.DNA40370    308 GGCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCC
*****
P_AAH15579    301 GGCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATG
*****
P_AAH15579    361 TATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
P_AAH15579    421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
P_AAH15579    481 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
*****
P_AAH15579    541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCTGTTGATTGCGTGCTCTCCT
*****
P_AAH15579    601 ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCTGTTGATTGCGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
*****
P_AAH15579    661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
*****
P_AAH15579    721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC

ss.DNA40370    788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
*****
P_AAH15579    781 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
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ss.DNA40370      848 TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
*****
P_AAH15579      841 TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC

ss.DNA40370      908 ACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
*****
P_AAH15579      901 ACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC

ss.DNA40370      968 TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAG
*****
P_AAH15579      961 TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAG

ss.DNA40370     1028 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
*****
P_AAH15579     1021 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA

ss.DNA40370     1088 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
*****
P_AAH15579     1081 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC

ss.DNA40370     1148 TCATCGTAGATACCATGGGTCTGAGAGGCCTGGGTGCGGAACTGAAGTGCCAGAACTGC
*****
P_AAH15579     1141 TCATCGTAGATACCATGGGTCTGAGAGGCCTGGGTGCGGAACTGAAGTGCCAGAACTGC

ss.DNA40370     1208 CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
*****
P_AAH15579     1201 CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT

ss.DNA40370     1268 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
*****
P_AAH15579     1261 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA

ss.DNA40370     1328 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
*****
P_AAH15579     1321 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG

ss.DNA40370     1388 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
*****
P_AAH15579     1381 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA

ss.DNA40370     1448 GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCTGTATCTAACTGGGGCTGTGATCAAG
*****
P_AAH15579     1441 GGCCGCTGAAGCTGTAGGAAGCGCCACTCTTCCTGTATCTAACTGGGGCTGTGATCAAG

ss.DNA40370     1508 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
*****
P_AAH15579     1501 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT

ss.DNA40370     1568 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGGATCAAAA
*****
P_AAH15579     1561 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGGATCAAAA

ss.DNA40370     1628 TAAAGGATGATAATAGATATT
*****
P_AAH15579     1621 TAAAGGATGATAATAGATATT

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>22 P_ABV28721 Human prostate expression marker cDNA 28712. (1973 bp) [1 seg]

Score = 1637 (3245 bits), Expect = 0.0
Identities = 1637/1637 (100%), at 13,32-1649,1668, Strand +/-

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ss.DNA40370      13 TGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGG
*****
P_ABV28721       32 TGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGG

ss.DNA40370      73 TTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACA
*****
P_ABV28721       92 TTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACA

ss.DNA40370     133 GAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
*****
P_ABV28721     152 GAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG

ss.DNA40370     193 TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG
*****
P_ABV28721     212 TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG

ss.DNA40370     253 CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCC
*****
P_ABV28721     272 CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCC

ss.DNA40370     313 CTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTT
*****
P_ABV28721     332 CTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTT

ss.DNA40370     373 GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCATGCCAAG
*****
P_ABV28721     392 GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCATGCCAAG

ss.DNA40370     433 GACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCAC
*****
P_ABV28721     452 GACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCAC

ss.DNA40370     493 AAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCA
*****
P_ABV28721     512 AAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCA

ss.DNA40370     553 GCTGGCATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTT
*****
P_ABV28721     572 GCTGGCATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTT

ss.DNA40370     613 GCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGA
*****
P_ABV28721     632 GCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGA

ss.DNA40370     673 CCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTT
*****
P_ABV28721     692 CCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTT

ss.DNA40370     733 GCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGG
*****
P_ABV28721     752 GCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGG

ss.DNA40370     793 GGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTA
*****
P_ABV28721     812 GGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTA
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ss.DNA40370	853	ACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTA

P_ABV28721	872	ACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTA
ss.DNA40370	913	GTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATG

P_ABV28721	932	GTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATG
ss.DNA40370	973	AATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAG

P_ABV28721	992	AATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAG
ss.DNA40370	1033	GCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTG

P_ABV28721	1052	GCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTG
ss.DNA40370	1093	GACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATC

P_ABV28721	1112	GACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATC
ss.DNA40370	1153	GTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAA

P_ABV28721	1172	GTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAA
ss.DNA40370	1213	TTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCT

P_ABV28721	1232	TTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCT
ss.DNA40370	1273	TTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTT

P_ABV28721	1292	TTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTT
ss.DNA40370	1333	CCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG

P_ABV28721	1352	CCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG
ss.DNA40370	1393	GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCG

P_ABV28721	1412	GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCG
ss.DNA40370	1453	CTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGT

P_ABV28721	1472	CTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGT
ss.DNA40370	1513	TCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTT

P_ABV28721	1532	TCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTT
ss.DNA40370	1573	CTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAG

P_ABV28721	1592	CTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAG
ss.DNA40370	1633	GATGATAATAGATATTA

P_ABV28721	1652	GATGATAATAGATATTA

>23 AK027373 Homo sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly (1641 bp) [1 seg]

Score = 1637 (3245 bits), Expect = 0.0

Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/+

```
ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
      AK027373      1 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
      AK027373     61 GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
      AK027373    121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
      AK027373    181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGAACTTTGAGGAAATTG
      AK027373    241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGAACTTTGAGGAAATTG

ss.DNA40370    308 GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC
      AK027373    301 GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATG
      AK027373    361 TATTTGTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
      AK027373    421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
      AK027373    481 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
      AK027373    541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTGCTCTCCT
      AK027373    601 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
      AK027373    661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
      AK027373    721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC

ss.DNA40370    788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACA
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AK027373	781	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACA
ss.DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
AK027373	841	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
AK027373	901	ACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
AK027373	961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
AK027373	1021	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
AK027373	1081	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
AK027373	1141	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
ss.DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
AK027373	1201	CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
AK027373	1261	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
AK027373	1321	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
AK027373	1381	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
AK027373	1441	GGCCGCTGAAGCTGTAGGAAGCGCCACTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
AK027373	1501	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
AK027373	1561	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATT
AK027373	1621	TAAAGGATGATAATAGATATT

>24 BD157571 Primer for synthesizing full-length cDNA and use thereof. (1641 bp)
[1 seg]

Score = 1637 (3245 bits), Expect = 0.0

Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/-

```
ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
   BD157571      1 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
   BD157571     61 GGTGGTTGCTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
   BD157571    121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
   BD157571    181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTG
   BD157571    241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTG

ss.DNA40370    308 GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC
   BD157571    301 GGCCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG
   BD157571    361 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
   BD157571    421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAA
   BD157571    481 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
   BD157571    541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
   BD157571    601 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
   BD157571    661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
   BD157571    721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
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ss.DNA40370	788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA

BD157571	781	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
ss.DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC

BD157571	841	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC

BD157571	901	ACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG

BD157571	961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA

BD157571	1021	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC

BD157571	1081	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTCTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGC

BD157571	1141	TCATCGTAGATACCATGGGTCTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGC
ss.DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT

BD157571	1201	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA

BD157571	1261	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG

BD157571	1321	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA

BD157571	1381	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG

BD157571	1441	GGCCGCTGAAGCTGTAGGAAGCGCCACTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT

BD157571	1501	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA

BD157571	1561	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATT

BD157571 1621 TAAAGGATGATAATAGATATT

>25 P_AAH72787 Human cervical cancer marker nucleic acid 4061. (1977 bp) [1 seg]
Score = 1633 (3237 bits), Expect = 0.0
Identities = 1633/1633 (100%), at 17,40-1649,1672, Strand +/-

```
ss.DNA40370 17 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC
*****
P_AAH72787 40 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC

ss.DNA40370 77 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGG
*****
P_AAH72787 100 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGG

ss.DNA40370 137 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC
*****
P_AAH72787 160 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC

ss.DNA40370 197 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTTCATGTGGCTTC
*****
P_AAH72787 220 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTTCATGTGGCTTC

ss.DNA40370 257 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCTTG
*****
P_AAH72787 280 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCTTG

ss.DNA40370 317 ACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG
*****
P_AAH72787 340 ACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG

ss.DNA40370 377 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC
*****
P_AAH72787 400 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC

ss.DNA40370 437 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
*****
P_AAH72787 460 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG

ss.DNA40370 497 AATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG
*****
P_AAH72787 520 AATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG

ss.DNA40370 557 GCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGG
*****
P_AAH72787 580 GCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGG

ss.DNA40370 617 GGGTTGCCTTGGGTGATTCTGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTT
*****
P_AAH72787 640 GGGTTGCCTTGGGTGATTCTGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTT

ss.DNA40370 677 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG
*****
P_AAH72787 700 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG

ss.DNA40370 737 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
*****
P_AAH72787 760 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
```

ss.DNA40370	797	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA *****
P_AAH72787	820	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA
ss.DNA40370	857	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT *****
P_AAH72787	880	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT
ss.DNA40370	917	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG *****
P_AAH72787	940	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG
ss.DNA40370	977	GCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTA *****
P_AAH72787	1000	GCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTA
ss.DNA40370	1037	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG *****
P_AAH72787	1060	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG
ss.DNA40370	1097	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG *****
P_AAH72787	1120	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG
ss.DNA40370	1157	ATACCATGGGTTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCA *****
P_AAH72787	1180	ATACCATGGGTTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCA
ss.DNA40370	1217	GTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG *****
P_AAH72787	1240	GTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG
ss.DNA40370	1277	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT *****
P_AAH72787	1300	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT
ss.DNA40370	1337	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG *****
P_AAH72787	1360	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG
ss.DNA40370	1397	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA *****
P_AAH72787	1420	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA
ss.DNA40370	1457	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG *****
P_AAH72787	1480	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG
ss.DNA40370	1517	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC *****
P_AAH72787	1540	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC
ss.DNA40370	1577	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG *****
P_AAH72787	1600	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG
ss.DNA40370	1637	ATAATAGATATTA *****

P_AAH72787 1660 ATAATAGATATTA

>26 AX188369 Sequence 4064 from Patent WO0142467. DNA, linear, PAT 06-AUG-2001 (1977 bp) [1 seg]

Score = 1633 (3237 bits), Expect = 0.0

Identities = 1633/1633 (100%), at 17,40-1649,1672, Strand +/+

```
ss.DNA40370 17 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC
*****
AX188369 40 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC

ss.DNA40370 77 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCCACAGAGG
*****
AX188369 100 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCCACAGAGG

ss.DNA40370 137 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC
*****
AX188369 160 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC

ss.DNA40370 197 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGGCTTC
*****
AX188369 220 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGGCTTC

ss.DNA40370 257 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCCTTG
*****
AX188369 280 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCCTTG

ss.DNA40370 317 ACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG
*****
AX188369 340 ACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG

ss.DNA40370 377 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC
*****
AX188369 400 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC

ss.DNA40370 437 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
*****
AX188369 460 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG

ss.DNA40370 497 AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG
*****
AX188369 520 AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG

ss.DNA40370 557 GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG
*****
AX188369 580 GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG

ss.DNA40370 617 GGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTT
*****
AX188369 640 GGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTT

ss.DNA40370 677 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG
*****
AX188369 700 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG

ss.DNA40370 737 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
*****
AX188369 760 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
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ss.DNA40370 797 AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA

 AX188369 820 AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA

ss.DNA40370 857 AAAGCACTCCCACGTCTACAATGGAGTCGAGCTAGAATTCACACAGAGCCACCTAGTTT

 AX188369 880 AAAGCACTCCCACGTCTACAATGGAGTCGAGCTAGAATTCACACAGAGCCACCTAGTTT

ss.DNA40370 917 GTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG

 AX188369 940 GTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG

ss.DNA40370 977 GCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTA

 AX188369 1000 GCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTA

ss.DNA40370 1037 CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG

 AX188369 1060 CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG

ss.DNA40370 1097 AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG

 AX188369 1120 AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG

ss.DNA40370 1157 ATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCA

 AX188369 1180 ATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCA

ss.DNA40370 1217 GTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG

 AX188369 1240 GTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG

ss.DNA40370 1277 TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTT

 AX188369 1300 TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTT

ss.DNA40370 1337 CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG

 AX188369 1360 CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG

ss.DNA40370 1397 GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA

 AX188369 1420 GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA

ss.DNA40370 1457 AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG

 AX188369 1480 AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG

ss.DNA40370 1517 ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC

 AX188369 1540 ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC

ss.DNA40370 1577 TTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG

 AX188369 1600 TTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG

ss.DNA40370 1637 ATAATAGATATTA

AX188369 1660 ATAATAGATATTA

>27 P_AAD12590 Human protein having hydrophobic domain encoding cDNA clone
HP03959. (1897 bp) [1 seg]

Score = 1619 (3209 bits), Expect = 0.0

Identities = 1622/1623 (99%), at 27,1-1649,1623, Strand +/-

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ss.DNA40370      27  ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC
*****
P_AAD12590        1  ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC

ss.DNA40370      87  GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGA
*****
P_AAD12590       61  GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGA

ss.DNA40370     147  AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC
*****
P_AAD12590     121  AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC

ss.DNA40370     207  CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCC
*****
P_AAD12590     181  CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCC

ss.DNA40370     267  AGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCTTGACAGTGATCT
*****
P_AAD12590     241  AGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCTTGACAGTGATCT

ss.DNA40370     327  CAAACCACGGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT
*****
P_AAD12590     301  CAAACCACGGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT

ss.DNA40370     387  GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT
*****
P_AAD12590     361  GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT

ss.DNA40370     447  GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC
*****
P_AAD12590     421  GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC

ss.DNA40370     507  AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT
*****
P_AAD12590     481  AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT

ss.DNA40370     567  AGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT
*****
P_AAD12590     541  AGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT

ss.DNA40370     627  GGGTGATTCTGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG
*****
P_AAD12590     601  GGGTGATTCTGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG

ss.DNA40370     687  CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT
*****
P_AAD12590     661  CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT

ss.DNA40370     747  GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
*****
```

P_AAD12590	721	GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
ss.DNA40370	807	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCC

P_AAD12590	781	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCC
ss.DNA40370	867	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA

P_AAD12590	841	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA
ss.DNA40370	927	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG

P_AAD12590	901	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG
ss.DNA40370	987	AAAGAAGCTCAAAATTATTCTTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT

P_AAD12590	961	AAAGAAGCTCAAAATTATTCTTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT
ss.DNA40370	1047	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA

P_AAD12590	1021	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA
ss.DNA40370	1107	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG

P_AAD12590	1081	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG
ss.DNA40370	1167	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAA

P_AAD12590	1141	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAA
ss.DNA40370	1227	GTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTA

P_AAD12590	1201	GTGGAAGGCCCTGTACAGTGACCCTAAATCTCTGGAACATCTGCTTTTGTCAAGTCCTA
ss.DNA40370	1287	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTTCTGACCAAGG

P_AAD12590	1261	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTTCTGACCAAGG
ss.DNA40370	1347	GGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTG

P_AAD12590	1321	GGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTG
ss.DNA40370	1407	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA

P_AAD12590	1381	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA
ss.DNA40370	1467	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT

P_AAD12590	1441	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT
ss.DNA40370	1527	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA

P_AAD12590	1501	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA
ss.DNA40370	1587	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA

P_AAD12590	1561	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA

ss.DNA40370 1647 TTA

P_AAD12590 1621 TTA

>28 AX191563 Sequence 85 from Patent WO0149728. DNA, linear, PAT 15-AUG-2001
(1897 bp) [1 seg]

Score = 1619 (3209 bits), Expect = 0.0

Identities = 1622/1623 (99%), at 27,1-1649,1623, Strand +/+

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ss.DNA40370 27 ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC
*****
AX191563 1 ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC

ss.DNA40370 87 GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCACTGGCCACAGAGGAGGGCAAGGA
*****
AX191563 61 GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCACTGGCCACAGAGGAGGGCAAGGA

ss.DNA40370 147 AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC
*****
AX191563 121 AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC

ss.DNA40370 207 CACCAACTCCTGCAAGAAGCTTCTCAGAACTGCCCTGGTCATGTGGCTTCAGGGCGGTCC
*****
AX191563 181 CACCAACTCCTGCAAGAAGCTTCTCAGAACTGCCCTGGTCATGTGGCTTCAGGGCGGTCC

ss.DNA40370 267 AGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCCTTGACAGTGATCT
*****
AX191563 241 AGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCCTTGACAGTGATCT

ss.DNA40370 327 CAAACCACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT
*****
AX191563 301 CAAACCACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT

ss.DNA40370 387 GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT
*****
AX191563 361 GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT

ss.DNA40370 447 GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC
*****
AX191563 421 GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC

ss.DNA40370 507 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT
*****
AX191563 481 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT

ss.DNA40370 567 AGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT
*****
AX191563 541 AGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT

ss.DNA40370 627 GGGTGATTCTGGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG
*****
AX191563 601 GGGTGATTCTGGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG

ss.DNA40370 687 CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT
*****
AX191563 661 CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT

ss.DNA40370 747 GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
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AX191563	721	GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
ss.DNA40370	807	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC

AX191563	781	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC
ss.DNA40370	867	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA

AX191563	841	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA
ss.DNA40370	927	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG

AX191563	901	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG
ss.DNA40370	987	AAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT

AX191563	961	AAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT
ss.DNA40370	1047	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA

AX191563	1021	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA
ss.DNA40370	1107	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG

AX191563	1081	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG
ss.DNA40370	1167	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAA

AX191563	1141	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAA
ss.DNA40370	1227	GTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTA

AX191563	1201	GTGGAAGGCCCTGTACAGTGACCCTAAATCTCTGGAACATCTGCTTTTGTCAAGTCCTA
ss.DNA40370	1287	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG

AX191563	1261	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG
ss.DNA40370	1347	GGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTG

AX191563	1321	GGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTG
ss.DNA40370	1407	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA

AX191563	1381	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA
ss.DNA40370	1467	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT

AX191563	1441	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT
ss.DNA40370	1527	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA

AX191563	1501	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA
ss.DNA40370	1587	AACCTAAGATTTTTTAAAAAATTGATTGTGTTTGTATCAAAATAAAGGATGATAATAGATA

AX191563	1561	AACCTAAGATTTTTTAAAAAATTGATTGTGTTTGTATCAAAATAAAGGATGATAATAGATA

ss.DNA40370 1647 TTA

AX191563 1621 TTA

>29 AF113214 Homo sapiens MSTP034 mRNA, complete cds. (1902 bp) [1 seg]
Score = 1594 (3160 bits), Expect = 0.0
Identities = 1594/1594 (100%), at 56,1-1649,1594, Strand +/-

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ss.DNA40370 56 CTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTG
*****
AF113214 1 CTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTG

ss.DNA40370 116 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
*****
AF113214 61 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG

ss.DNA40370 176 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
*****
AF113214 121 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC

ss.DNA40370 236 TGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGT
*****
AF113214 181 TGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGT

ss.DNA40370 296 TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGG
*****
AF113214 241 TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGG

ss.DNA40370 356 CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTA
*****
AF113214 301 CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTA

ss.DNA40370 416 GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
*****
AF113214 361 GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA

ss.DNA40370 476 CTTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
*****
AF113214 421 CTTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT

ss.DNA40370 536 ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGA
*****
AF113214 481 ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGA

ss.DNA40370 596 CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATT
*****
AF113214 541 CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATT

ss.DNA40370 656 CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG
*****
AF113214 601 CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG

ss.DNA40370 716 CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
*****
AF113214 661 CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG

ss.DNA40370 776 AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
```

AF113214	721	***** AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
ss.DNA40370	836	ACTTCTATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAAT *****
AF113214	781	ACTTCTATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAAT
ss.DNA40370	896	TCACACAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATG *****
AF113214	841	TCACACAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATG
ss.DNA40370	956	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATC *****
AF113214	901	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATC
ss.DNA40370	1016	AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC *****
AF113214	961	AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
ss.DNA40370	1076	CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG *****
AF113214	1021	CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
ss.DNA40370	1136	GACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGT *****
AF113214	1081	GACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGT
ss.DNA40370	1196	GGCCAGAAGTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAAT *****
AF113214	1141	GGCCAGAAGTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAAT
ss.DNA40370	1256	CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA *****
AF113214	1201	CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA
ss.DNA40370	1316	AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG *****
AF113214	1261	AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
ss.DNA40370	1376	TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA *****
AF113214	1321	TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
ss.DNA40370	1436	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG *****
AF113214	1381	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
ss.DNA40370	1496	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG *****
AF113214	1441	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
ss.DNA40370	1556	CAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTG *****
AF113214	1501	CAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTG
ss.DNA40370	1616	TTTGTATCAAAATAAAGGATGATAATAGATATTA *****
AF113214	1561	TTTGTATCAAAATAAAGGATGATAATAGATATTA

>30 P_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. (1921 bp) [1 seg]

Score = 1543 (3059 bits), Expect = 0.0

Identities = 1619/1642 (98%), Gaps = 3/1642 (0%), at 8,2-1649,1640, Strand +/-

```
ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
*****
P_AAC75884       2 GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
*****
P_AAC75884      62 GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
*****
P_AAC75884     122 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA
*****
P_AAC75884     182 TCTGGTGGCTCTATTATGCCACCA-CTCCTGCAAGAACTTC--AGAACTGCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
*****
P_AAC75884     239 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG

ss.DNA40370    308 GGCCCTTGACAGTGATCTCAAACCACGAAACCACCTGGCTCCAGGCTGCCAGTCTCC
*****
P_AAC75884     299 GGCCCTTGACAGTGATCTCAAACCACGAAACCACCTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG
*****
P_AAC75884     359 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
P_AAC75884     419 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
P_AAC75884     479 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
*****
P_AAC75884     539 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTCGGTGCTCTCCT
*****
P_AAC75884     599 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTCGGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
*****
P_AAC75884     659 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
*****
P_AAC75884     719 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
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ss.DNA40370 788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA

 P_AAC75884 779 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
 ss.DNA40370 848 TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTACACACAGAGCC

 P_AAC75884 839 TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTACACACAGAGCC
 ss.DNA40370 908 ACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC

 P_AAC75884 899 ACCTAGTTTGTCTCTGTCAGCGCCACGTGAGACACCTACAACGAGACGCCTTAAGCCAGC
 ss.DNA40370 968 TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG

 P_AAC75884 959 TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
 ss.DNA40370 1028 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
 ***** **
 P_AAC75884 1019 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATCGACA
 ss.DNA40370 1088 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC

 P_AAC75884 1079 TTGTGGATACGTTGCTGGAGGCAGGGGTCAATGTGACTGTGTATAATGGGCAGCTGGATC
 ss.DNA40370 1148 TCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
 **** *
 P_AAC75884 1139 TCATTGTGGACACCATAGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGT
 ss.DNA40370 1208 CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
 * *
 P_AAC75884 1199 CCAGATTCAATCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
 ss.DNA40370 1268 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA

 P_AAC75884 1259 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
 ss.DNA40370 1328 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG

 P_AAC75884 1319 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
 ss.DNA40370 1388 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA

 P_AAC75884 1379 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
 ss.DNA40370 1448 GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG

 P_AAC75884 1439 GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
 ss.DNA40370 1508 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT

 P_AAC75884 1499 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
 ss.DNA40370 1568 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA

 P_AAC75884 1559 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
 ss.DNA40370 1628 TAAAGGATGATAATAGATATTA

P_AAC75884 1619 TAAAGGATGATAATAGATATTA

>31 P_ABK30363 Human G-protein-coupled protease #133. cDNA, PAT 23-APR-2002
(1960 bp) [1 seg]

Score = 1407 (2789 bits), Expect = 0.0

Identities = 1620/1658 (97%), Gaps = 26/1658 (1%), at 17,11-1649,1667, Strand
+ / +

```
ss.DNA40370 17 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGT-GGTTG
***** ** **
P_ABK30363 11 GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGAAGGATG

ss.DNA40370 76 CTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAG
*****
P_ABK30363 71 CTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAG

ss.DNA40370 136 GAGGGCAAGG--AAGTAT-GGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
***** * ***
P_ABK30363 131 GAGGGCAAGGGAACCTTATGGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG

ss.DNA40370 193 TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCATGTGG
*****
P_ABK30363 191 TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCATGTGG

ss.DNA40370 253 CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCC
*****
P_ABK30363 251 CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCC

ss.DNA40370 313 CTTGACAGTGATCTCAAACCAC-GGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATT
*****
P_ABK30363 311 CTTGACAGTGATCTCAAACCACGGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATT

ss.DNA40370 372 TGTGGATAATCCCGT-GGGCACTGGGTTTCACTTATGTGAATGGT-AGTGGTGCCTATGCC
*****
P_ABK30363 371 TGTGGATAATCCCGTAGGGCACTGGGTTTCACTTATGTGAATGGTAAGTGGTGCCTATGCC

ss.DNA40370 430 AAGGACCTGGC-TATGGTGGCTTCAGACAT-GATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
P_ABK30363 431 AAGGACCTGGCTTATGGTGGCTTCAGACATGGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370 488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
P_ABK30363 491 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370 548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
*****
P_ABK30363 551 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370 608 ACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTGGTGTCTCCT
*****
P_ABK30363 611 ACTTTGCGGGGGTTGCCTTGGGTGAATCCTGGATCTCCCCTGTTGATTGGTGTCTCCT

ss.DNA40370 668 GGGGACC-TTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCT
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P_ABK30363 671 GGGGACCATTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCT

ss.DNA40370 727 AAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAG
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P_ABK30363 731 AAGGTTGCAGAGCAAGT-CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAG
ss.DNA40370 787 CTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTA-TAA

P_ABK30363 790 CTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATTAA
ss.DNA40370 846 CATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTC-TAGAATTCACACAGA

P_ABK30363 850 CATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCCTAGAATTCACACAGA
ss.DNA40370 905 GCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTG-AGACACCTACAACGAGATGCCTTAAGC

P_ABK30363 910 GCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAAGACACCTTACACGAGATGCCTTAAGC
ss.DNA40370 964 CAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGG

P_ABK30363 970 CAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGG
ss.DNA40370 1024 GGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATT

P_ABK30363 1030 GGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATT
ss.DNA40370 1084 AGCATTGTGGA-CGAGTTGCTGGAGGCAGGGATCAA-CGTGA-CGGTGTA-TAATGGAC-
***** * *****
P_ABK30363 1090 AGCATTGTGGACCAAGTTGCTGGAGGCAGGGATCAACCGTGACCGGTGTATTAATGGACA
ss.DNA40370 1139 AGC-TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGG
*** *****
P_ABK30363 1150 AGCTTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGG
ss.DNA40370 1198 CCAGAACTGCCTAAATTCAGTCAGCTGAAGT-GGAAGGCCCTGTACAGTGACCCTAAATC

P_ABK30363 1210 CCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGGAAGGCCCTGTACAGTGACCCTAAATC
ss.DNA40370 1257 TTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAA

P_ABK30363 1270 TTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAA
ss.DNA40370 1317 AGCTGGTCATATGGTTCCTTCTGACCAA-GGGGACATGGCTCTGAAGATGATGAGACTGG

P_ABK30363 1330 AGCTGGTCATATGGTTCCTTCTGACCAAGGGGGACATGGCTCTGAAGATGATGAGACTGG
ss.DNA40370 1376 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTT-TGGCCTTGGGGCAC

P_ABK30363 1390 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTATGGCCTTGGGGCAC
ss.DNA40370 1435 AGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAAC-TG

P_ABK30363 1450 AGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTTG
ss.DNA40370 1494 GGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCA-TTGTCTCTGG

P_ABK30363 1510 GGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGG
ss.DNA40370 1553 AGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAA-TTGA

P_ABK30363 1570 AGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGA

ss.DNA40370 1612 TTTGTTTTGATCAAAATAAAGGATGATAATAGATATTA
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P_ABK30363 1630 TTCGTTTCGATCAAAATAAAGGATGATAATAGATATTA

>32 P_AAH89926 Human bone marrow cDNA, SEQ ID NO: 57. cDNA, PAT 01-OCT-2001
(1940 bp) [1 seg]
Score = 1389 (2753 bits), Expect = 0.0
Identities = 1577/1629 (96%), Gaps = 13/1629 (0%), at 34,10-1649,1638, Strand
+/+

ss.DNA40370 34 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG

P_AAH89926 10 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCTGTGGTTGCTGGAGCTGCCGCTGCTA
ss.DNA40370 94 CTGGGCCTGAACGCAAGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG

P_AAH89926 70 CTGGGCCTGAACGCAAGAGCTGTCATTGACTGCCCCACAGAGGAGGGCAAGGAACCATGG
ss.DNA40370 154 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC

P_AAH89926 130 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGGTATATTATGCCACCAAC
ss.DNA40370 214 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT
* *****
P_AAH89926 190 TTCTGCAAGAACTTTTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTGCAGGCGGT
ss.DNA40370 274 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCA

P_AAH89926 250 TCTAACACTGGATTTGGAACTCTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCA
ss.DNA40370 334 CGGAAAACCACTGG-----CTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGG

P_AAH89926 310 CGGAAAACCACTGGGTACACTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGG
ss.DNA40370 389 GCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCC-TATGCCAAGGACCTGGCTATGGTG

P_AAH89926 370 GCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCCTATGCCAAGGACCTGGCTATGGTG
ss.DNA40370 448 GCTTCAGACATGATGG-TTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC

P_AAH89926 430 GCTTCAGACATGATGGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC
ss.DNA40370 507 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT

P_AAH89926 490 AGTTCCATTGTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT
ss.DNA40370 567 AGAGCTTTATAAGGCCATTTCAGCGAGGGACC-ATCAAGTGCAACTTTGCGGGGGTTGCCT

P_AAH89926 550 AGAGCTTTATAAGGCCATTTCAGCGAGGGACCCATAAAGTGCAACTTTGCGGGGGTTGCCT
ss.DNA40370 626 TGGGTGATTCTGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACA

P_AAH89926 610 TGGGTGATTCTGAACTCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACA
ss.DNA40370 686 GCATGTCTCTT-CTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA

P_AAH89926 670 GCATGTCTCTTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA

ss.DNA40370	745	CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAA
P_AAH89926	730	CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAA
ss.DNA40370	805	ATGATCATTGAACAGAACACAGATGGGGTGAAC TTCTATAACATCTTA ACTAAAAGCACT
P_AAH89926	790	ATGATCATTGAACAGAACACAGATGGGGTGAAC TTCTATAACATCTTA ACTAAAAGCACT
ss.DNA40370	865	CCCACGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGT
P_AAH89926	850	CCCACGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGT
ss.DNA40370	925	CAGCGCCACGTGAGACACCTACAACGAGATGC-CTTAAGCC-AGCTCATGAATGGCCCCA
P_AAH89926	910	CAGCGCCACGTGAGACACCTACAACGATATGCACCTAAGCCTATTTTCATGAACGGCCCCA
ss.DNA40370	983	TCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACG
P_AAH89926	970	TCAAAAAGAAACCCAAAATTATTCTGACGATCCTTCCTGGGTAGGCCAGGCTACCAACG
ss.DNA40370	1043	TCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGC
P_AAH89926	1030	TCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTACATTGTGGACGAGTTGC
ss.DNA40370	1103	TGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCA
P_AAH89926	1090	TGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCA
ss.DNA40370	1163	TGGGTCAAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGC
P_AAH89926	1150	TGGGTCAAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGC
ss.DNA40370	1223	TGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGT
P_AAH89926	1210	TGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGT
ss.DNA40370	1283	CCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTTCTGACC
P_AAH89926	1270	CCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTTCCTTCTGACC
ss.DNA40370	1343	AAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGG
P_AAH89926	1330	AAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGG
ss.DNA40370	1403	GCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGT
P_AAH89926	1390	GCTGGAGATGAGCCGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGT
ss.DNA40370	1463	AGGAAGCGCCATTCTTCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGC
P_AAH89926	1450	AGGAAGCGCCATTCTTCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGC
ss.DNA40370	1523	TTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTA
P_AAH89926	1510	TTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTA
ss.DNA40370	1583	AAAAAA-CCTAAGA-TTTTTTAAAAAATTGATTGTTTTTGATCAAAATAAAGGATGATAA

P_AAH89926 1570 AAAAAACCCTAAGATTTTTTTAAAAAATTGATTATTTTGGATCAAACCAAAGGATGATAA
ss.DNA40370 1641 TAGATATTA

P_AAH89926 1630 TAGATATTA

>33 AX191553 Sequence 75 from Patent WO0149728. DNA, linear, PAT 15-AUG-2001
(1359 bp) [1 seg]
Score = 1355 (2686 bits), Expect = 0.0
Identities = 1358/1359 (99%), at 34,1-1392,1359, Strand +/+

ss.DNA40370 34 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG

AX191553 1 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG
ss.DNA40370 94 CTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG

AX191553 61 CTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG
ss.DNA40370 154 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC

AX191553 121 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC
ss.DNA40370 214 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT

AX191553 181 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT
ss.DNA40370 274 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCA

AX191553 241 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCA
ss.DNA40370 334 CGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT

AX191553 301 CGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT
ss.DNA40370 394 GGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA

AX191553 361 GGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA
ss.DNA40370 454 GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCA

AX191553 421 GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCA
ss.DNA40370 514 TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT

AX191553 481 TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT
ss.DNA40370 574 TATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT

AX191553 541 TATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT
ss.DNA40370 634 TCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT

AX191553 601 TCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT
ss.DNA40370 694 CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC

AX191553 661 CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC

ss.DNA40370	754	GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT

AX191553	721	GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT
ss.DNA40370	814	GAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCACGTCT

AX191553	781	GAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCACGTCT
ss.DNA40370	874	ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGCCAC

AX191553	841	ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGCCAC
ss.DNA40370	934	GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG

AX191553	901	GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG
ss.DNA40370	994	CTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC

AX191553	961	CTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC
ss.DNA40370	1054	ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG

AX191553	1021	ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG
ss.DNA40370	1114	ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAG

AX191553	1081	ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAG
ss.DNA40370	1174	GCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAG

AX191553	1141	GCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAG
ss.DNA40370	1234	GCCCTGTACAGTGACCCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC

AX191553	1201	GCCCTGTACAGTGACCCCTAAATCTCTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC
ss.DNA40370	1294	CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG

AX191553	1261	CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG
ss.DNA40370	1354	GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG

AX191553	1321	GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG

GenBank (Release 134, feb 2003)

P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. 650 bp,
cDNA, PAT 29-MAY-2001

ACCESSION P_AAF30502

KEYWORDS PRO302; vitellogenic carboxypeptidase homologue; human;
angiogenesis; cardiovascularisation; trauma; wound; cancer;
atherosclerosis; cardiac hypertrophy; macular degeneration;
cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
antirheumatic; antiarthritic; antiinflammatory; vulnerary;
antitumour; diagnosis; gene therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong,S., Gerritsen,M.E., Goddard,A., Gurney,A.L., Hillan,K.J.
Williams,P.M., Wood,W.I.

TITLE Composition comprising a PRO230, PRO216 or PRO302 polypeptide,
agonist or antagonist for promoting or inhibiting angiogenesis
and/or cardiovascularisation in mammals -

JOURNAL Patent: WO200119987-A1; Filing Date: 29-NOV-1999; 99WO-US28214;
Publication Date: 22-MAR-2001; Priority: 13-SEP-1999;
99WO-US20944. 15-SEP-1999; 99WO-US21090; Assignee: (GETH)
GENENTECH INC; Cross Reference: WPI; 2001-235264/24. P-PSDB;
AAB20341; Patent Format: Claim 56; Fig 5; 141pp; English.

COMMENT The present sequence is that of cDNA clone DNA40370-1217 (ATCC
209485) encoding human PRO302 (see AAB20341), a vitellogenic
carboxypeptidase homologue. The cDNA was isolated following
expressed sequence tag database searches using extracellular domains
of about 950 known secreted sequences, use of isolated sequences to
design PCR primers and probe (see AAF30509-12), screening of cDNA
libraries, and isolation from a foetal lung tissue library. PRO302
is 1 of 3 novel PRO proteins of the invention. PRO230, PRO216 and
PRO302 polynucleotides and polypeptides, recombinant retroviral
particles, ex vivo producer cells, expression vectors, host cells,
and methods of recombinant production are provided, as well as
antibodies, agonists and antagonists. The polynucleotides,
polypeptides, agonists and antagonists are useful for treating or
diagnosing a cardiovascular, endothelial or angiogenic disorder in a
mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related
macular degeneration (all claimed), atherosclerosis, hypertension,
arterial restenosis, rheumatoid arthritis, angina, myocardial
infarction, thrombophlebitis and lymphangitis. The polypeptides,
agonists and antagonists are also used in claimed methods of
stimulating or inhibiting endothelial cell growth.

FEATURES Location/Qualifiers

CDS 34..1392

/*tag= a

sig_peptide 34..108

/*tag= b

mat_peptide 109..1389

/*tag= c

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

P_AAA13199 PRO302, vitellogenic carboxypeptidase homologue nucleotide sequence.
650 bp, cDNA, PAT 20-JUL-2000

ACCESSION P_AAA13199

KEYWORDS Human; PRO302; Vitellogenic carboxypeptidase; cardiant; angiogenic;

cytostatic; ophthalmic; antiproliferative activity; ss;
cardiovascular; endothelial; angiogenic disorder; cardiac
hypertrophy; trauma; cancer; myocardial infarction; age-related
macular degeneration; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong,S., Gerritsen,M.E., Goddard,A., Gurney,A.L., Hillan,K.J.
Williams,P.M., Wood,W.I.

TITLE A composition comprising PRO230, PRO216 or PRO302 polypeptides,
agonists or antagonists useful for promotion or inhibition of
cardiovascularisation, angiogenesis or endothelialisation in mammals

JOURNAL Patent: WO200015792-A2; Filing Date: 13-SEP-1999; 99WO-US20944;
Publication Date: 23-MAR-2000; Priority: 14-SEP-1998;
98US-0100262. 14-SEP-1998; 98WO-US19177; Assignee: (GETH)
GENENTECH INC; Cross Reference: WPI; 2000-271431/23; Patent Format:
Example 3; Fig 5; 135pp; English.

COMMENT This sequence represents the nucleotide sequence encoding a human
PRO302 protein. PRO302 is a human vitellogenic carboxypeptidase
homologue. The invention relates to a composition comprising a
PRO230 (tubulointerstitial nephritis antigen homologue), PRO216
(osteomodulin/fibromodulin homologue) or PRO302 (vitellogenic
carboxypeptidase homologue) polypeptide, or an agonist or antagonist
of these. Also included in the invention is a method for preparing
the composition, agonists and antagonists of PRO230, PRO216 or
PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302
polypeptides. The composition of the invention has cardiant,
angiogenic, cytostatic, ophthalmic, and antiproliferative activity.
Analysis of the level of expression of a gene encoding a PRO230,
PRO216 or PRO302 polypeptide or detecting the presence/absence of
the polypeptide is useful for diagnosis of cardiovascular,
endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216
or PRO302 antibodies are useful in these diagnostic methods. The
PRO230, PRO216 or PRO302 polypeptides (and their coding sequences),
agonists and antagonists are useful for treatment of cardiovascular,
endothelial or angiogenic disorders, especially cardiac hypertrophy
(especially characterized by presence of an elevated level of
PGF-2alpha), trauma or cancer, myocardial infarction or age-related
macular degeneration. In particular, PRO216, an agonist of PRO216,
an antagonist of PRO230, PRO216 or PR302 or an anti-PRO216 antibody
is useful for inhibition of endothelial cell growth in a mammal.
Endothelial cell growth can be stimulated by administration of
PRO230, a PRO230 agonist or antagonist or an anti-PRO230 antibody.
Additionally, an anti-PRO302 antibody can inhibit angiogenesis
induced by PRO302 in a mammal.

FEATURES

CDS

Location/Qualifiers

34..1392

/*tag= a

/product= PRO302

/note= "Vitellogenic carboxypeptidase homologue"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. 650 bp,
DNA, PAT 25-JUN-1999

ACCESSION P_AAX52258

KEYWORDS Secreted protein; transmembrane protein; human; enterocolitis;

Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Chen, J., Goddard, A., Gurney, A.L., Pennica, D., Wood, W.I., Yuan, J.

TITLE New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

JOURNAL Patent: WO9914328-A2; Filing Date: 16-SEP-1998; 98WO-US19330; Publication Date: 25-MAR-1999; Priority: 25-NOV-1997;

97US-0066840. 17-SEP-1997; 97US-0059113. 17-SEP-1997;
97US-0059115. 17-SEP-1997; 97US-0059117. 17-SEP-1997;
97US-0059119. 17-SEP-1997; 97US-0059121. 17-SEP-1997;
97US-0059122. 17-SEP-1997; 97US-0059184. 18-SEP-1997;
97US-0059263. 18-SEP-1997; 97US-0059266. 15-OCT-1997;
97US-0062125. 17-OCT-1997; 97US-0062285. 17-OCT-1997;
97US-0062287. 21-OCT-1997; 97US-0063486. 24-OCT-1997;
97US-0062814. 24-OCT-1997; 97US-0062816. 24-OCT-1997;
97US-0063045. 24-OCT-1997; 97US-0063120. 24-OCT-1997;
97US-0063121. 24-OCT-1997; 97US-0063127. 24-OCT-1997;
97US-0063128. 27-OCT-1997; 97US-0063329. 27-OCT-1997;
97US-0063327. 28-OCT-1997; 97US-0063541. 28-OCT-1997;
97US-0063542. 28-OCT-1997; 97US-0063544. 28-OCT-1997;
97US-0063549. 28-OCT-1997; 97US-0063550. 28-OCT-1997;
97US-0063564. 29-OCT-1997; 97US-0063435. 29-OCT-1997;
97US-0063704. 29-OCT-1997; 97US-0063732. 29-OCT-1997;
97US-0063738. 29-OCT-1997; 97US-0063734. 29-OCT-1997;
97US-0064215. 29-OCT-1997; 97US-0063735. 31-OCT-1997;
97US-0063870. 31-OCT-1997; 97US-0064103. 03-NOV-1997;
97US-0064248. 07-NOV-1997; 97US-0064809. 12-NOV-1997;
97US-0065186. 17-NOV-1997; 97US-0065846. 18-NOV-1997;
97US-0065693. 21-NOV-1997; 97US-0066120. 21-NOV-1997;
97US-0066364. 24-NOV-1997; 97US-0066772. 24-NOV-1997;
97US-0066466. 24-NOV-1997; 97US-0066770. 24-NOV-1997;
97US-0066511. 24-NOV-1997; 97US-0066453; Assignee: (GETH)
GENENTECH INC; Cross Reference: WPI; 1999-229533/19. P-PSDB;
AAY13387; Patent Format: Claim 2; Fig 89; 320pp; English.

COMMENT AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g.

for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

FEATURES Location/Qualifiers
 BASE COUNT 414 a 365 c 453 g 418 t
 ORIGIN

P AAX25445 Human PRO216 cDNA clone UNQ265. 650 bp, cDNA, PAT 19-JUL-1999

ACCESSION P AAX25445

KEYWORDS PRO302; vitellogenic carboxypeptidase; human; angiogenesis; cardiovascularisation; wound healing; cancer; atherosclerosis; cardiac hypertrophy; myocardial infarction; antiangiogenic; antitumour; tissue regeneration; pulmonary fibrosis; neurological disease; macular degeneration; diagnosis; therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong, S., Gerritsen, M.E., Goddard, A., Gurney, A.L., Hillan, K. Williams, P.M., W. Odwi;

TITLE Composition containing human polypeptides with anti-angiogenic activity

JOURNAL Patent: WO9914234-A2; Filing Date: 14-SEP-1998; 98WO-US19177; Publication Date: 25-MAR-1999; Priority: 24-NOV-1997; 97US-0066772. 17-SEP-1997; 97US-0059117. 27-OCT-1997; 97US-0063329; Assignee: (GETH) GENENTECH INC; Cross Reference: WPI; 1999-254381/21. P-PSDB; AAY05768; Patent Format: Example 1; Fig 8; 102pp; English.

COMMENT This is the DNA sequence of human cDNA clone UNQ265 or DNA40370-1217 (ATCC 209485), which encodes PRO302, identified as a vitellogenic carboxypeptidase homologue (see AAY05768). The cDNA clone was isolated from a human foetal kidney tissue cDNA library using a probe and primers (see AAX25456-59) based on a consensus sequence (see AAX25449) for PRO302 that had been deduced from a set of overlapping EST clones (see AAX25446-48). Compositions containing PRO302, PRO216 (human osteomodulin, see AAY05767) and PRO230 in admixture with a carrier are claimed. The compositions are used to treat or prevent a wide range of cardiovascular, endothelial and angiogenic disorders (claimed), specifically cardiac hypertrophy (especially where associated with elevated levels of prostaglandin F2 alpha or induced by myocardial infarction), trauma (wounds, burns, or tissue regeneration more generally, including neurological disease), and cancer. Antagonists may be used similarly, also to treat age-related macular degeneration (or other angiogenic retinal disorders) and to prevent excessive growth of connective tissue during wound healing or in pulmonary fibrosis.

FEATURES Location/Qualifiers
 CDS 34..1392
 /*tag= a
 sig_peptide 34..108
 /*tag= b
 mat_peptide 109..1289
 /*tag= c

BASE COUNT 414 a 365 c 453 g 418 t
ORIGIN

— P AAF72416 Human PRO302 cDNA. 650 bp, cDNA, PAT 24-APR-2001

ACCESSION P_AAF72416

KEYWORDS Human; PRO; dermatological; antipsoriatic; cytostatic;
antiinflammatory; antiparkinsonian nootropic; neuroprotective;
vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic;
antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic;
antiviral; diabetes; ophthalmological; gene therapy; skin disease;
gastrointestinal disorder; ischaemia; inflammation; patent; GENESEQ
patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

0 AUTHORS Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L.,
Ferrara,N. Filvaroff,E., Fong,S., Gao,W., Gerber,H.,
Gerritsen,M.E., Goddard,A. Godowski,P.J., Grimaldi,C.J.,
Gurney,A.L., Hillan,K.J., Kljavin,I.J. Mather,J.P., Pan,J.,
Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D. Williams,P.M.,
Wood,W.I.

TITLE Sixty one nucleic acids encoding PRO polypeptides which are useful
in the treatment of skin diseases (e.g. psoriasis), cancers (e.g.
lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
Alzheimer's disease) -

JOURNAL Patent: WO200104311-A1; Filing Date: 22-FEB-2000; 2000WO-US04414;
Publication Date: 18-JAN-2001; Priority: 07-JUL-1999;
99US-0143048. 26-JUL-1999; 99US-0145698. 28-JUL-1999;
99US-0146222. 08-SEP-1999; 99WO-US20594. 13-SEP-1999;
99WO-US20944. 15-SEP-1999; 99WO-US21090. 15-SEP-1999;
99WO-US21547. 05-OCT-1999; 99WO-US23089. 29-NOV-1999;
99WO-US28214. 30-NOV-1999; 99WO-US28313. 16-DEC-1999;
99WO-US30095. 20-DEC-1999; 99WO-US30911. 20-DEC-1999;
99WO-US30999. 05-JAN-2000; 99WO-US00219; Assignee: (GETH)
GENENTECH INC; Cross Reference: WPI; 2001-081051/09. P-PSDB;
AAB80255; Patent Format: Claim 2; Fig 89; 393pp; English.

COMMENT The present sequence is one of sixty one nucleic acids encoding
novel secreted and transmembrane PRO polypeptides. The PRO
polypeptides are useful for treating skin diseases (e.g. psoriasis),
cancers (e.g. lung squamous cell carcinoma), gastrointestinal
disorders (e.g. enterocolitis), neurodegenerative diseases (e.g.
Alzheimer's disease, Parkinson's disease), wound repair,
cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
ischaemias such as coronary ischaemia, atherosclerosis),
inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple
sclerosis), infertility, AIDS and diabetes and retinal disorders
such as retinitis pigmentosum. The PRO nucleic acids have
applications in molecular biology, including use as hybridization
probes, and in chromosome and gene mapping.

FEATURES Location/Qualifiers

BASE COUNT 414 a 365 c 453 g 418 t
ORIGIN

— P ABL95586 Human angiogenesis related cDNA PRO302 SEQ ID NO: 51. 650 bp,
cDNA, PAT 19-JUL-2002

ACCESSION P_ABL95586

KEYWORDS Human; angiogenesis; PRO protein; cardiovascularisation; wound;
cancer; atherosclerosis; cardiac hypertrophy; gene therapy;

endothelial disorder; cardiant; cytostatic; antiangiogenic;
hypotensive; vulnerary; antiarteriosclerotic; gene; patent; GENESEQ
patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.F., Watanabe, C.K., Williams, P.M., Wood, W.I.,
Ye, W.

TITLE One hundred and eighty seven nucleic acids encoding PRO
polypeptides, useful in diagnosis and treatment of cardiovascular
(e.g. myocardial infarction), endothelial or angiogenic disorders in
a mammal -

JOURNAL Patent: WO200208284-A2; Filing Date: 09-JUL-2001; 2001WO-US21735;
Publication Date: 31-JAN-2002; Priority: 20-JUL-2000;
2000US-219556P. 25-JUL-2000; 2000US-220624P. 25-JUL-2000;
2000US-220664P. 28-JUL-2000; 2000WO-US20710. 02-AUG-2000;
2000US-222695P. 17-AUG-2000; 2000US-0643657. 23-AUG-2000;
2000WO-US23522. 24-AUG-2000; 2000WO-US23328. 07-SEP-2000;
2000US-230978P. 15-SEP-2000; 2000US-000000P. 18-SEP-2000;
2000US-0664610. 18-SEP-2000; 2000US-0665350. 24-OCT-2000;
2000US-242922P. 08-NOV-2000; 2000US-0709238. 08-NOV-2000;
2000WO-US30952. 10-NOV-2000; 2000WO-US30873. 01-DEC-2000;
2000WO-US32678. 20-DEC-2000; 2000US-0747259. 20-DEC-2000;
2000WO-US34956. 22-JAN-2001; 2001US-0767609. 28-FEB-2001;
2001US-0796498. 28-FEB-2001; 2001WO-US06520. 01-MAR-2001;
2001WO-US06666. 09-MAR-2001; 2001US-0802706. 14-MAR-2001;
2001US-0808689. 22-MAR-2001; 2001US-0816744. 05-APR-2001;
2001US-0828366. 10-MAY-2001; 2001US-0854208. 10-MAY-2001;
2001US-0854280. 25-MAY-2001; 2001US-0866028. 25-MAY-2001;
2001US-0866034. 25-MAY-2001; 2001WO-US17092. 30-MAY-2001;
2001US-0870574. 30-MAY-2001; 2001WO-US17443. 01-JUN-2001;
2001WO-US17800. 20-JUN-2001; 2001WO-US19692. 28-JUN-2001;
2001WO-US00000; Assignee: (GETH) GENENTECH INC. (BAKE/) BAKER K P.
(FERR/) FERRARA N. (GERB/) GERBER H. (GERR/) GERRITSEN M E. (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (HILL/) HILLAN K J. (MARS/) MARSTERS S A. (PANJ/) PAN J. (PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C K. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I; Cross Reference: WPI; 2002-171999/22. P-PSDB; ABB95448;
Patent Format: Claim 1; Fig 51; 567pp; English.

COMMENT The present invention provides the protein and coding sequences of
human PRO proteins. These are useful for treating or diagnosing a
cardiovascular, endothelial or angiogenic disorder, including
cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
rheumatoid arthritis, angina, myocardial infarctions,
thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
carcinoma and liver carcinoma) and wound healing. The present
sequence is a coding sequence of the invention.

FEATURES Location/Qualifiers

BASE COUNT 414 a 365 c 453 g 418 t
ORIGIN

P_ABL88097 Human PRO302 cDNA sequence SEQ ID NO:51. 650 bp,
cDNA, PAT 16-MAY-2002

ACCESSION P_ABL88097

KEYWORDS Human; angiogenesis; cardiant; cytostatic; antiangiogenic;

hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A. Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F. Stephan, J.F., Watanabe, C.K., Williams, P.M., Wood, W.I., Ye, W.

TITLE One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

JOURNAL Patent: WO200200690-A2; Filing Date: 20-JUN-2001; 2001WO-US19692; Publication Date: 03-JAN-2002; Priority: 23-JUN-2000; 2000US-213637P. 20-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-220624P. 25-JUL-2000; 2000US-220664P. 28-JUL-2000; 2000WO-US20710. 02-AUG-2000; 2000US-222695P. 17-AUG-2000; 2000US-0643657. 23-AUG-2000; 2000WO-US23522. 24-AUG-2000; 2000WO-US23328. 07-SEP-2000; 2000US-230978P. 18-SEP-2000; 2000US-0664610. 18-SEP-2000; 2000US-0665350. 24-OCT-2000; 2000US-242922P. 08-NOV-2000; 2000US-0709238. 08-NOV-2000; 2000WO-US30952. 10-NOV-2000; 2000WO-US30873. 01-DEC-2000; 2000WO-US32678. 20-DEC-2000; 2000US-0747259. 20-DEC-2000; 2000WO-US34956. 22-JAN-2001; 2001US-0767609. 28-FEB-2001; 2001US-0796498. 28-FEB-2001; 2001WO-US06520. 01-MAR-2001; 2001WO-US06666. 09-MAR-2001; 2001US-0802706. 14-MAR-2001; 2001US-0808689. 22-MAR-2001; 2001US-0816744. 05-APR-2001; 2001US-0828366. 10-MAY-2001; 2001US-0854208. 10-MAY-2001; 2001US-0854280. 25-MAY-2001; 2001US-0866028. 25-MAY-2001; 2001US-0866034. 25-MAY-2001; 2001WO-US17092. 30-MAY-2001; 2001US-0870574. 30-MAY-2001; 2001WO-US17443. 01-JUN-2001; 2001WO-US17800; Assignee: (GETH) GENENTECH INC; Cross Reference: WPI; 2002-090516/12. P-PSDB; ABB84842; Patent Format: Claim 2; Fig 51; 565pp; English.

COMMENT ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiatic, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

FEATURES Location/Qualifiers

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

AX098272 Sequence 11 from Patent WO0119987. 1650 bp,
DNA, linear, PAT 02-APR-2001

ACCESSION AX098272

VERSION AX098272.1 GI:13537577

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Fong, S., Gerritsen, M.E., Goddard, A., Gurney, A.L., Hillan, K.J.,
Williams, P.M. and Wood, W.I.

TITLE Promotion or inhibition of angiogenesis and cardiovascularization

JOURNAL Patent: WO 0119987-A 11 22-MAR-2001;

Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..1650

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/db_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

AX454466 Sequence 51 from Patent WO0208284. 1650 bp,
DNA, linear, PAT 06-JUL-2002

ACCESSION AX454466

VERSION AX454466.1 GI:21713857

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 51 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

BD075577 Secretory and transmembrane polypeptide and nucleic acid encoding
the same. 1650 bp, DNA, linear, PAT 27-AUG-2002

ACCESSION BD075577

VERSION BD075577.1 GI:22621180
 KEYWORDS JP 2001516580-A/210.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
 TITLE Secretory and transmembrane polypeptide and nucleic acid encoding
 the same
 JOURNAL Patent: JP 2001516580-A 210 02-OCT-2001;
 GENENTECH INC
 COMMENT OS Homo sapiens (human)
 PN JP 2001516580-A/210
 PD 02-OCT-2001
 PF 16-SEP-1998 JP 2000511867
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 25-NOV-1997 US 60/066840
 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
 JEAN CHEN,
 PI JEAN YUAN
 PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
 PC C12N1/19,
 PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02// (C12P21/08, PC
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 PC C12N15/00,C12N5/00
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FEATURES Location/Qualifiers
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              the same. 1650 bp, DNA, linear, PAT 18-FEB-2003
ACCESSION     BD173394
VERSION       BD173394.1  GI:28414705
KEYWORDS      JP 2002238588-A/210.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 1650)
AUTHORS       Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
              Yuan,J.
TITLE         Secreted and transmembrane polypeptides and nucleic acids encoding
              the same
JOURNAL       Patent: JP 2002238588-A 210 27-AUG-2002;
              GENENTECH INC
COMMENT       OS Homo sapiens (human)
              PN JP 2002238588-A/210
              PD 27-AUG-2002
              PF 18-DEC-2001 JP 2001385315
              PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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              WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
              JIAN ZHENG,
              PI JEAN YUAN
              PC C12N15/09,C07K14/435,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
              C12N5/10,
              PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
              PC (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
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 BASE COUNT 414 a 365 c 453 g 418 t
 ORIGIN

BD173075 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same. 1650 bp, DNA, linear, PAT 18-FEB-2003

ACCESSION BD173075
 VERSION BD173075.1 GI:28414384
 KEYWORDS JP 2002238587-A/210.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood, W. I., Gurney, A. L., Goddard, A., Pennica, D., Zheng, J. and
 Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same

JOURNAL Patent: JP 2002238587-A 210 27-AUG-2002;
 GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002238587-A/210

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385248

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
 JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC

C12N15/02,
 PC
 C12P21/02,C12P21/08// (C12P21/02,C12R1:91), (C12P21/02,C12R1:19), PC
 (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted
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AX490944 Sequence 51 from Patent WO0200690. 1650 bp,
 DNA, linear, PAT 16-AUG-2002
 ACCESSION AX490944
 VERSION AX490944.1 GI:22323809
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
 Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
 and Ye,W.
 TITLE Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 JOURNAL Patent: WO 0200690-A 51 03-JAN-2002;
 Genentech, Inc. (US)
 FEATURES Location/Qualifiers
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 ORIGIN

BD172756 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same. 1650 bp, DNA, linear, PAT 18-FEB-2003
 ACCESSION BD172756
 VERSION BD172756.1 GI:28414060
 KEYWORDS JP 2002238586-A/210.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1650)
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
 Yuan,J.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: JP 2002238586-A 210 27-AUG-2002;
 GENENTECH INC
 COMMENT OS Homo sapiens (human)

PN JP 2002238586-A/210
 PD 27-AUG-2002
 PF 18-DEC-2001 JP 2001385205
 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
 WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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 PI JEAN YUAN
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BD172437 Secreted and transmembrane polypeptides and nucleic acids encoding
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 ACCESSION BD172437
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 KEYWORDS JP 2002223786-A/210.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1650)
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: JP 2002223786-A 210 13-AUG-2002; GENENTECH INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002223786-A/210
 PD 13-AUG-2002
 PF 18-DEC-2001 JP 2001385135
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 WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
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 C12N5/10,
 PC
 C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC
 (C12P21/02,C12R1:645),C12N15/00,C12N5/00
 CC Secreted and transmembrane polypeptides and nucleic CC acids
 encoding the same
 FH Key Location/Qualifiers
 FT source 1..1650
 FT /organism='Homo sapiens (human)'.
 FEATURES Location/Qualifiers
 source 1..1650
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 414 a 365 c 453 g 418 t
 ORIGIN
 BD175428 Secretory and transmembrane polypeptide and nucleic acid encoding

the same. 1650 bp, DNA, linear, PAT 18-MAR-2003

ACCESSION BD175428

VERSION BD175428.1 GI:29121126

KEYWORDS JP 2002253280-A/210.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.

TITLE Secretory and transmembrane polypeptide and nucleic acid encoding
the same

JOURNAL Patent: JP 2002253280-A 210 10-SEP-2002;
GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002253280-A/210

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR

31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
A61P25/00,

PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,

PC C07K19/00,

PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,

PC A61P43/00,

PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,

PC C12R1:91),

PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC

Secretory and transmembrane polypeptide and nucleic acid CC
encoding the same

FH	Key	Location/Qualifiers
FT	source	1..1650
FT		/organism='Homo sapiens (human)'

FEATURES

	Location/Qualifiers
source	1..1650
	/organism="Homo sapiens"
	/db_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

— P ABV72656 Human retinoid inducible serine carboxypeptidase cDNA. 921 bp,
cDNA, PAT 29-NOV-2002

ACCESSION P ABV72656

KEYWORDS Serine carboxypeptidase; mammalian; RISC; antihypertensive; retinoid-inducible serine carboxypeptidase; antiarteriosclerotic; nephrotropic; antiasthmatic; vasotropic; gene therapy; vascular disease; vascular hyperplasia; atherosclerosis; restenosis; glomerulonephritis; hypertension; obstructive bladder disease; tubulosclerosis; asthma; interstitial tubular disease; human; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS Miano, J.M., Streb, J.W., Chen, J.

TITLE New retinoid-inducible serine carboxypeptidase proteins and nucleic acids, useful for detecting or treating vascular diseases, e.g. vascular hyperplasia, atherosclerosis, asthma, glomerulonephritis, hypertension -

JOURNAL Patent: WO200268599-A2; Filing Date: 22-FEB-2002; 2002WO-US05560; Publication Date: 06-SEP-2002; Priority: 22-FEB-2001; 2001US-271183P. 23-MAY-2001; 2001US-293097P; Assignee: (UYRP) UNIV ROCHESTER; Cross Reference: WPI; 2002-713371/77. P-PSDB; ABB99215; Patent Format: Disclosure; Page 21-22; 129pp; English.

COMMENT The invention relates to a novel mammalian retinoid-inducible serine carboxypeptidase (RISC) protein or polypeptide. The proteins of the invention have antiarteriosclerotic, antihypertensive, nephrotropic, antiasthmatic, and vasotropic activity. The polynucleotides of the invention may have a use in gene therapy. The retinoid-inducible serine carboxypeptidase protein and the nucleic acid molecule are useful in detecting, preventing or treating vascular diseases or disorders, e.g. vascular hyperplasia, atherosclerosis, restenosis, glomerulonephritis, hypertension, obstructive bladder disease, tubulosclerosis, asthma or interstitial tubular disease, in inhibiting smooth muscle cell growth and inhibiting the activity of extracellular regulated kinase. The transgenic animal is useful in screening and identifying agents that induce or suppress the function of the retinoid-inducible genes. The sequence encodes the human RISC of the invention.

FEATURES	Location/Qualifiers
5'UTR	1..32
	/*tag= b
CDS	33..1391
	/*tag= a
	/product= "RISC"
3'UTR	1391..1921
	/*tag= c

BASE COUNT 502 a 412 c 486 g 521 t

ORIGIN

P_ABV77921 Hypoxia-induced protein coding sequence #35. 921 bp,
DNA, PAT 12-NOV-2002

ACCESSION P_ABV77921

KEYWORDS Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene
therapy; antiinflammatory; vulnerary; gynecological;
ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis;
apoptosis; cancer; ischaemic condition; reperfusion injury;
retinopathy; neonatal stress; preeclampsia; atherosclerosis;
inflammatory condition; wound healing; inflammation; erythropoiesis;
hair loss; human; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS White,J., Mundy,C.R., Ward,N.R., Krige,D., Kingsman,S.M.,
Harris,R.A. Rayner,W.N.

TITLE Identifying a gene involved in disease for treating
hypoxia-regulated conditions, comprises comparing the
transcriptome/proteome of two cell types under different conditions
and identifying a differentially regulated gene -

JOURNAL Patent: WO200246465-A2; Filing Date: 10-DEC-2001; 2001WO-GB05458;
Publication Date: 13-JUN-2002; Priority: 08-DEC-2000;
2000GB-0030076. 08-FEB-2001; 2001GB-0003156. 25-OCT-2001;
2001GB-0025666; Assignee: (OXFO-) OXFORD BIOMEDICA UK LTD; Cross
Reference: WPI; 2002-627238/67; Patent Format: Claim 23; Page 306;
538pp; English.

COMMENT The present invention relates to methods for identifying genes and
proteins that are implicated in a specific disease or physiological
condition. The method comprises comparing the transcriptome/proteome
of a specialised cell type implicated in a disease or condition with
that of a second specialised cell type, under two experimental
conditions, and identifying a gene that is differentially regulated
in the two specialised cell types under experimental conditions.
ABV77873-ABV78116 and ABP65061-ABP65257 were identified using the
methods of the invention. The coding sequences and proteins are
useful for treating a disease in a patient, for manufacture of a
medicament for treating hypoxia-regulated conditions, and for
regulating tumourigenesis, angiogenesis, apoptosis, biological
response to hypoxia conditions, or hypoxic-associated pathology in a
patient. The coding sequences and proteins are also useful for
monitoring the therapeutic treatment of a disease or physiological
condition, such as cancer, ischaemic conditions, reperfusion injury,
retinopathy, neonatal stress, preeclampsia, atherosclerosis,
inflammatory conditions, wound healing, inflammation, erythropoiesis
or hair loss.

FEATURES Location/Qualifiers

BASE COUNT 502 a 413 c 487 g 519 t

ORIGIN

AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
mRNA, complete cds. 1921 bp, mRNA, linear, PRI 27-SEP-2000

ACCESSION AF282618

VERSION AF282618.1 GI:10312168

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1921)
 AUTHORS Cho, J.-J. and Baik, H.-H.
 TITLE Cloning of novel serine carboxypeptidase precursor
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1921)
 AUTHORS Cho, J.-J. and Baik, H.-H.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-2000) Microbiology, Kyung Hee University, Hoeki
 1, Seoul 130-701, Korea
 FEATURES Location/Qualifiers
 source 1..1921
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="17"
 /map="between hRPC1107_A_17 and hRPK.166_P_13"
 gene 1..1921
 /gene="HSCP1"
 CDS 33..1391
 /gene="HSCP1"
 /codon_start=1
 /product="serine carboxypeptidase 1 precursor protein"
 /protein_id="AAG16692.1"
 /db_xref="GI:10312169"
 BASE COUNT 502 a 413 c 487 g 519 t
 ORIGIN

NM_021626 Homo sapiens likely homolog of rat and mouse retinoid-inducible
 serine carboxypeptidase (RISC), mRNA. 1921 bp,
 mRNA, linear, PRI 23-DEC-2002
 ACCESSION NM_021626
 VERSION NM_021626.1 GI:11055991
 KEYWORDS REFSEQ; RISC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1921)
 AUTHORS Chen, J., Streb, J.W., Maltby, K.M., Kitchen, C.M. and Miano, J.M.
 TITLE Cloning of a novel retinoid-inducible serine carboxypeptidase from
 vascular smooth muscle cells
 JOURNAL J. Biol. Chem. 276 (36), 34175-34181 (2001)
 MEDLINE 21424023
 PUBMED 11447226
 REFERENCE 2 (bases 1 to 1921)
 AUTHORS Cho, J.-J. and Baik, H.-H.
 TITLE Cloning of novel serine carboxypeptidase precursor
 JOURNAL Unpublished
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from AF282618.1.
 FEATURES Location/Qualifiers
 source 1..1921
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="17"
 /map="17q23.1"
 gene 1..1921
 /gene="RISC"
 /note="synonym: HSCP1"

/db_xref="LocusID:59342"
 CDS 33..1391
 /gene="RISC"
 /codon_start=1
 /product="serine carboxypeptidase 1 precursor protein"
 /protein_id="NP_067639.1"
 /db_xref="GI:11055992"
 /db_xref="LocusID:59342"
 misc_feature 156..1370
 /gene="RISC"
 /note="serine_carbpept; Region: Serine carboxypeptidase"
 /db_xref="CDD:pfam00450"
 misc_feature 171..1379
 /gene="RISC"
 /note="COG2939; Region: Carboxypeptidase C (cathepsin A)
 [Amino acid transport and metabolism]"
 /db_xref="CDD:COG2939"
 BASE COUNT 502 a 413 c 487 g 519 t
 ORIGIN

P_AAH15579 Human cDNA sequence SEQ ID NO:13881. 641 bp, cDNA, PAT 26-JUN-2001

ACCESSION P_AAH15579

KEYWORDS Human; primer; detection; diagnosis; antisense therapy; gene therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1641)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K.,
 Yamamoto,J. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K.,
 Otsuki,T.

TITLE Primer sets for synthesizing polynucleotides, particularly the 5602
 full-length cDNAs defined in the specification, and for the
 detection and/or diagnosis of the abnormality of the proteins
 encoded by the full-length cDNAs -

JOURNAL Patent: EP1074617-A2; Filing Date: 28-JUL-2000; 2000EP-0116126;
 Publication Date: 07-FEB-2001; Priority: 29-JUL-1999;
 99JP-0248036. 27-AUG-1999; 99JP-0300253. 11-JAN-2000;
 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000;
 2000JP-0241899; Assignee: (HELI-) HELIX RES INST; Cross Reference:
 WPI; 2001-318749/34; Patent Format: Claim 8; SEQ ID 13881; 2537pp +
 CD ROM; English.

COMMENT The present invention describes primer sets for synthesising 5602
 full-length cDNAs defined in the specification. Where a primer set
 comprises: (a) an oligo-dT primer and an oligonucleotide
 complementary to the complementary strand of a polynucleotide which
 comprises one of the 5602 nucleotide sequences defined in the
 specification, where the oligonucleotide comprises at least 15
 nucleotides; or (b) a combination of an oligonucleotide comprising a
 sequence complementary to the complementary strand of a
 polynucleotide which comprises a 5'-end sequence and an
 oligonucleotide comprising a sequence complementary to a
 polynucleotide which comprises a 3'-end sequence, where the
 oligonucleotide comprises at least 15 nucleotides and the
 combination of the 5'-end sequence/3'-end sequence is selected from
 those defined in the specification. The primer sets can be used in
 antisense therapy and in gene therapy. The primers are useful for
 synthesising polynucleotides, particularly full-length cDNAs. The
 primers are also useful for the detection and/or diagnosis of the

abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

FEATURES Location/Qualifiers
BASE COUNT 412 a 364 c 451 g 414 t
ORIGIN

— P_ABV28721 Human prostate expression marker cDNA 28712. 973 bp,
cDNA, PAT 16-SEP-2002

ACCESSION P_ABV28721

KEYWORDS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic
marker; pharmacogenomic marker; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1973)

AUTHORS Schlegel, R., Endege, W.O., Monahan, J.E.

TITLE Novel isolated nucleic acid molecule associated with cancerous state
of prostate cells and correlating with presence of prostate cancer,
useful for detecting presence of prostate cancer, stage of prostate
cancer -

JOURNAL Patent: WO200160860-A2; Filing Date: 20-FEB-2001; 2001WO-US05171;
Publication Date: 23-AUG-2001; Priority: 17-FEB-2000;
2000US-183319P. 16-MAR-2000; 2000US-189862P. 25-MAY-2000;
2000US-207454P. 09-JUN-2000; 2000US-211314P. 18-JUL-2000;
2000US-219007P. 13-DEC-2000; 2000US-255281P; Assignee: (MILL-)
MILLENNIUM PREDICTIVE MEDICINE INC; Cross Reference: WPI;
2001-662795/76; Patent Format: Claim 1; Page 6030-6031; 11750pp;
English.

COMMENT The invention relates to an isolated nucleic acid molecule (I)
comprising a nucleotide sequence given in Tables 1-9
(ABV00010-ABV62213) of the specification or its complement. (I) is
useful for: (a) assessing whether a patient is afflicted with
prostate cancer; (b) monitoring the progression of prostate cancer
in a patient; (c) assessing the efficacy of a test compound to
inhibit prostate cancer in a patient; (d) assessing the efficacy of
a therapy for inhibiting prostate cancer in a patient; (e) selecting
a composition for inhibiting prostate cancer in a patient; (f)
assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a
patient; (h) assessing the aggressiveness or indolence of prostate
cancer in a patient; (I) is also useful as a pharmacodynamic or
pharmacogenomic marker.

FEATURES Location/Qualifiers
BASE COUNT 519 a 418 c 495 g 522 t 19 others
ORIGIN

— AK027373 Homo sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly similar
to VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-). 1641 bp,
mRNA, linear, PRI 01-AUG-2002

ACCESSION AK027373

VERSION AK027373.1 GI:14042005

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

○ AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1641)

AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES Location/Qualifiers

source 1..1641
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAMMA1000672"
/tissue_type="mammary gland"
/clone_lib="MAMMA1"
/note="cloning vector: pME18SFL3"

CDS 27..1385
/note="unnamed protein product"
/codon_start=1
/protein_id="BAB55069.1"
/db_xref="GI:14042006"

BASE COUNT 412 a 364 c 451 g 414 t

ORIGIN

— BD157571 Primer for synthesizing full-length cDNA and use thereof. 1641 bp,
DNA, linear, PAT 17-JAN-2003

ACCESSION BD157571

VERSION BD157571.1 GI:27863329

KEYWORDS JP 2002191363-A/12414.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1641)

○ AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 12414 09-JUL-2002;
HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/12414

PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
 10,
 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 Location/Qualifiers
 FT CDS (27)..(1382).
 FEATURES Location/Qualifiers
 source 1..1641
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 412 a 364 c 451 g 414 t
 ORIGIN

P_AAH72787 Human cervical cancer marker nucleic acid 4061. 977 bp,
 cDNA, PAT 19-SEP-2001

ACCESSION P_AAH72787

KEYWORDS Cervical cancer; cytostatic; pre-malignant condition; gene therapy;
 patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1977)

AUTHORS Schlegel, R., Deeds, J., Berger, A., Zhao, X.

TITLE New isolated nucleic acid for diagnosing and treating cervical
 cancer and for assessing and detecting compounds for treating the
 cancer -

JOURNAL Patent: WO200142467-A2; Filing Date: 08-DEC-2000; 2000WO-US33312;
 Publication Date: 14-JUN-2001; Priority: 08-DEC-1999;
 99US-0169681. 21-DEC-1999; 99US-0171350. 14-MAR-2000;
 2000US-0189315. 12-MAY-2000; 2000US-0203791. 09-JUN-2000;
 2000US-0210600. 21-JUL-2000; 2000US-0220114; Assignee: (MILL-)
 MILLENNIUM PREDICTIVE MEDICINE INC; Cross Reference: WPI;
 2001-375006/39; Patent Format: Claim 1; Page 853; 1051pp; English.

COMMENT The invention relates to novel genes (AAH68727-AAH73383) associated
 with cervical cancer with cytostatic activity. The nucleic acids and
 encoded polypeptides are useful: to assess if a patient is afflicted
 with cervical cancer or has a pre-malignant condition; to monitor
 the progression of cervical cancer or a premalignant condition in a
 patient; and to select and/or assess the efficacy of a compound or
 therapy for inhibiting cervical cancer in a patient. The nucleic
 acids may also be useful for gene therapy.

FEATURES Location/Qualifiers
 BASE COUNT 520 a 421 c 496 g 521 t 19 others
 ORIGIN

AX188369 Sequence 4064 from Patent WO0142467. 1977 bp,
 DNA, linear, PAT 06-AUG-2001

ACCESSION AX188369

VERSION AX188369.1 GI:15139842

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.

TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer

JOURNAL Patent: WO 0142467-A 4064 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers

source 1..1977
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 520 a 421 c 496 g 521 t 19 others

ORIGIN

P_AAD12590 Human protein having hydrophobic domain encoding cDNA clone HP03959.
897 bp, cDNA, PAT 25-SEP-2001

ACCESSION P_AAD12590

KEYWORDS Human; hydrophobic domain; gene therapy; nutritional supplement;
cell proliferation; immunomodulatory; autoimmune disorder;
antimicrobial; multiple sclerosis; rheumatoid arthritis;
insulin-dependent diabetes; haematopoiesis; tissue growth activity;
Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's
disease; chemotactic; chemokinetic; haemostatic; thrombolytic;
tumour growth inhibitor; anabolic; contraceptive; antiinfertility;
antiinflammatory; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1897)

AUTHORS Kato, S., Kimura, T.

TITLE Human proteins with hydrophobic domains and the nucleic acids
encoding them, useful for preventing diagnosing and treating e.g.
cancer, Alzheimer's and inflammation -

JOURNAL Patent: WO200149728-A2; Filing Date: 28-DEC-2000; 2000WO-JP09359;
Publication Date: 12-JUL-2001; Priority: 06-JAN-2000;
2000JP-0000585. 06-JAN-2000; 2000JP-0000588. 11-JAN-2000;
2000JP-0002299. 03-FEB-2000; 2000JP-0026862. 03-MAR-2000;
2000JP-0058367; Assignee: (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM
RES CENT; Cross Reference: WPI; 2001-418355/44. P-PSDB; AAE06595;
Patent Format: Claim 4; Page 410-413; 563pp; English.

COMMENT The present sequence is human protein with hydrophobic domain
encoding cDNA clone HP03959. The polynucleotide and polypeptide of
the invention may be used in the prevention, diagnosis and treatment
of diseases associated with inappropriate polypeptide expression.
The polynucleotides may be used to produce the polypeptide, by
inserting the nucleic acids into a host cell and culturing the cell
to express the protein. The polynucleotides and its complementary
sequences may also be used as DNA probes in diagnostic assays and
also used in gene therapy. The polypeptides may also be used as
antigens in the production of antibodies and in assays to identify
modulators of polypeptide expression and activity. The polypeptides
and nucleic acids may be used as nutritional supplements, to
modulate cytokine and cell proliferation activity, to modulate
immune stimulation or suppression (e.g. for the treatment of
microbial infections and autoimmune disorders such as multiple
sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to
modulate haematopoiesis, to modulate tissue growth activity (e.g.
for the treatment of Parkinson's disease, Huntington's disease and

Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.

FEATURES Location/Qualifiers
CDS 8..1366
 /*tag= a
 /product= "Human protein having hydrophobic domain"
 /note= "CDS is specifically is claimed in claim 3"
sig_peptide 8..88
 /*tag= b
mat_peptide 89..1363
 /*tag= c
 /product= "Mature human protein with hydrophobic domain"
BASE COUNT 499 a 406 c 477 g 515 t
ORIGIN

— AX191563 Sequence 85 from Patent WO0149728. 1897 bp,
 DNA, linear, PAT 15-AUG-2001

ACCESSION AX191563

VERSION AX191563.1 GI:15209749

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

0 AUTHORS Kato, S. and Kimura, T.

TITLE Human proteins having hydrophobic domains and dnas encoding these
 proteins

JOURNAL Patent: WO 0149728-A 85 12-JUL-2001;

Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)

FEATURES Location/Qualifiers

source 1..1897
 /organism="Homo sapiens"

CDS 8..1366
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC51169.1"
 /db_xref="GI:15209750"

BASE COUNT 499 a 406 c 477 g 515 t
ORIGIN

— AF113214 Homo sapiens MSTP034 mRNA, complete cds. 1902 bp,
 mRNA, linear, HTC 12-APR-2002

ACCESSION AF113214

VERSION AF113214.1 GI:11640575

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1902)

0 AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S.,
 Xu, Y.Y., Ye, J., Song, L., Gao, Y., Zhang, C.L., Zhang, J., Wei, Y.J.,
 Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y.,

Qiang,B.Q., Yuan,J.G., Liew,C.C., Zhao,M.S. and Hui,R.T.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
 Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
 Beijing 100037, P.R. China
 FEATURES Location/Qualifiers
 source 1..1902
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="aorta"
 CDS 129..1337
 /codon_start=1
 /product="MSTP034"
 /protein_id="AAG39285.1"
 /db_xref="GI:11640576"
 BASE COUNT 517 a 400 c 475 g 510 t
 ORIGIN

P_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. 921 bp,
CDNA, PAT 08-FEB-2001

ACCESSION P_AAC75884

KEYWORDS Human; open reading frame; ORFX; detection; cytostatic;
 hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic;
 neuroprotective; anticonvulsant; osteopathic; antiarthritic;
 immunosuppressant; cardiant; immunostimulant; thrombolytic;
 coagulant; vasotropic; antidiabetic; hypotensive; dermatological;
 immunosuppressive; antiinflammatory; antiviral; antibacterial;
 antifungal; antirheumatic; antithyroid; antianaemic; gene therapy;
 cancer; proliferative disorder; hypertension; neurodegenerative
 disorder; osteoarthritis; graft vs host disease; cardiovascular
 disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol
 ester storage; systemic lupus erythematosus; infection; severe
 combined immunodeficiency; malaria; autoimmune disorder; asthma;
 allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 bone damage; cartilage damage; antiinflammatory disease;
 coagulation; thrombosis; contraceptive; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS Shimkets,R.A., Leach,M.

TITLE Novel nucleic acids and peptides derived from open reading frame X,
 useful for treating e.g. cancers, proliferative disorders,
 neurodegenerative disorders and cardiovascular disease -

JOURNAL Patent: WO200058473-A2; Filing Date: 31-MAR-2000; 2000WO-US08621;
 Publication Date: 05-OCT-2000; Priority: 31-MAR-1999;
 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999;
 99US-0127728. 30-MAR-2000; 2000US-0540763; Assignee: (CURA-) CURAGEN
 CORP; Cross Reference: WPI; 2000-602362/57. P-PSDB; AAB41675; Patent
 Format: Claim 5; Page 2113-2115; 5507pp; English.

COMMENT AAC74446 to AAC77606 encode the proteins given in AAB40237.to
 AAB43397, which represent the human ORFX open reading frames 1 to
 3161. The ORFX sequences have activities such as: cytostatic;
 hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic;
 neuroprotective; osteopathic; anticonvulsant; antiarthritic;
 immunosuppressant; immunostimulant; cardiant; thrombolytic;
 coagulant; vasotropic; antidiabetic; hypotensive; dermatological;
 immunosuppressive; antiinflammatory; antibacterial; antiviral;
 antifungal; antirheumatic; antithyroid; and antianaemic. The

sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

FEATURES Location/Qualifiers
 BASE COUNT 506 a 411 c 485 g 518 t 1 others
 ORIGIN

P_ABK30363 Human G-protein-coupled protease #133. 960 bp,
 CDNA, PAT 23-APR-2002

ACCESSION P_ABK30363

KEYWORDS Human; ss; gene; G-protein-coupled protease; gene therapy;
 transgenic; protease mediated disorder; proliferative disorder;
 differentiative disorder; developmental disorder; haematopoietic
 disorder; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1960)

AUTHORS Robison, K.E.

TITLE New polynucleotides encoding protease homologs of the
 G-protein-coupled protease family, useful in identifying agonists
 and antagonists for diagnosis and treatment of protease mediated
 disorders -

JOURNAL Patent: US6331427-B1; Filing Date: 26-MAR-1999; 99US-0280116;
 Publication Date: 18-DEC-2001; Priority: 26-MAR-1999;
 99US-0280116; Assignee: (MILL-) MILLENNIUM PHARM INC; Cross
 Reference: WPI; 2002-129545/17; Patent Format: Disclosure; Column
 173-176; 246pp; English.

COMMENT The invention relates to an isolated human protease nucleic acid
 molecule comprising a nucleotide sequence of 546 base pairs, one of
 268 fully defined in the specification. Also disclosed are
 production of an isolated polypeptide encoded by the nucleic acid,
 comprising introducing the nucleic acid into a host cell and
 culturing under conditions to express the protein from the nucleic
 acid, use of an antibody to detect the encoded protein in a sample
 and to modulate its in vivo activity, identifying agents that bind
 to the protein and identification of a polynucleotide agent that
 modulates the expression of the nucleic acid or its complement (i.e.
 gene therapy). The nucleic acid can be used to identify an agent
 that modulates the expression or activity of the nucleic acid, and
 can be used to isolate the protein. The nucleic acid can be used in
 diagnostic assays for determining nucleic acid expression as well as
 activity in the context of a biological sample (e.g., blood, serum,
 cells, tissue) to determine whether an individual has a disease or
 disorder, or is at risk of developing a disease or disorder,
 associated with aberrant expression or activity of the nucleic acid.
 The nucleic acid can be used to detect mutations in protease genes
 and gene expression products such as mRNA. The nucleic acid can be

used as hybridisation probes to detect naturally-occurring genetic mutations in a protease gene. The nucleic acid can be used in drug screening methods to identify agonists and antagonists that can be used to diagnose and treat such protease mediated disorders e.g., proliferative, differentiative, developmental or haematopoietic disorders. The nucleic acid can be used as probes, primers, in biological assays, to determine patterns of gene expression, to design ribozymes and to construct transgenic animals. The present sequence represents one of the 268 disclosed human G-protein-coupled protease cDNA sequences.

FEATURES Location/Qualifiers
 BASE COUNT 525 a 418 c 493 g 524 t
 ORIGIN

— P_AAH89926 Human bone marrow cDNA, SEQ ID NO: 57. 940 bp,
 cDNA, PAT 01-OCT-2001

ACCESSION P_AAH89926

KEYWORDS Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
 antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 immunosuppressive; gene therapy; cytokine cell proliferation; cell
 differentiation modulator; immune disorder; infection; cancer; human
 immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
 patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1940)

AUTHORS Ford,J.E., Boyle,B.J., Tang,Y.T., Liu,C., Asundi,V., Chen,R.,
 Ma,Y. Ren,F., Wang,J., Werhman,T., Xu,C., Xue,A.J., Yang,Y.,
 Zhang,J. Zhao,Q.A., Zhou,P., Drmanac,R.T.

TITLE Novel bone-marrow-expressed polynucleotides and polypeptides, useful
 for treating e.g. cancer and immune deficiency disorders -

JOURNAL Patent: WO200153453-A2; Filing Date: 23-DEC-2000; 2000WO-US34960;
 Publication Date: 26-JUL-2001; Priority: 21-JAN-2000;
 2000US-0488725. 25-APR-2000; 2000US-0552317. 09-JUL-2000;
 2000US-0598042. 19-JUL-2000; 2000US-0620312. 03-AUG-2000;
 2000US-0653450. 14-SEP-2000; 2000US-0662191. 19-OCT-2000;
 2000US-0693036. 30-NOV-2000; 2000US-0250583; Assignee: (HYSE-) HYSEQ
 INC; Cross Reference: WPI; 2001-488707/53. P-PSDB; AAM00807; Patent
 Format: Claim 1; Page 244-245; 648pp; English.

COMMENT The present sequence is one of 251 novel human polynucleotides
 expressed in the bone marrow. The polynucleotide and the polypeptide
 encoded by it are useful in the treatment of various immune
 deficiencies and disorders. The deficiencies and disorders may be
 genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
 infection, or may result from an autoimmune disorder, a coagulation
 disorder (e.g. haemophilia), inhibition of tumour cell
 proliferation, suppression of an inflammatory response or treatment
 of a nervous system disorder such as Alzheimer's disease. Detection
 of the presence or increased expression of the polynucleotide or the
 protein it encodes is useful for the diagnosis and/or prognosis of
 one or more types of cancer. The polynucleotide and polypeptide can
 be used as nutritional sources or supplements and in the screening
 of chemical compounds as potential drugs.

FEATURES Location/Qualifiers
 BASE COUNT 537 a 410 c 469 g 524 t
 ORIGIN

— AX191553 Sequence 75 from Patent WO0149728. 1359 bp,

DNA, linear, PAT 15-AUG-2001
ACCESSION AX191553
VERSION AX191553.1 GI:15209735
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
proteins
JOURNAL Patent: WO 0149728-A 75 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES Location/Qualifiers
source 1..1359
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 337 a 318 c 375 g 329 t
ORIGIN